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OM protein - protein search, using bw model

Run on: May 5, 2005, 18:09:44 ; Search time: 28 Seconds
(without alignments)

Total number of hits satisfying chosen parameters: 272444

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cggn2_6/prodata/1/iaa/5A_COMB.pep:
2: /cggn2_6/prodata/1/iaa/5B_COMB.pep:
3: /cggn2_6/prodata/1/iaa/6A_COMB.pep:
4: /cggn2_6/prodata/1/iaa/6B_COMB.pep:
5: /cggn2_6/prodata/1/iaa/PCTUS_COMB.pep:
6: /cggn2_6/prodata/1/iaa/backfiles/pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	3 US-09-056-105-33	Sequence 33, Appl
2	11	100.0	11	3 US-09-025-585-1	Sequence 1, Appl
3	11	100.0	11	4 US-09-053-321-1	Sequence 1, Appl
4	11	100.0	11	4 US-08-556-416-1	Sequence 1, Appl
5	5	45.5	25	3 US-09-443-50A-1	Sequence 1, Appl
6	7	5	45.5	38	2 US-08-905-85
7	8	5	45.5	38	3 US-08-481-995B-85
8	9	5	45.5	41	4 US-09-493-795B-316
9	10	4	36.4	5	6 S217869-73
10	11	4	36.4	5	6 S227466-25
11	12	4	36.4	5	6 S217869-73
12	13	4	36.4	5	6 S227466-25
13	14	4	36.4	8	1 US-08-079-741A-101
14	15	4	36.4	8	1 US-07-339-05A-101
15	16	4	36.4	8	3 US-08-688-988-48
16	17	4	36.4	9	1 US-08-036-555B-27
17	18	4	36.4	9	1 US-08-469-559-27
18	19	4	36.4	9	1 US-08-249-322A-27
19	20	4	36.4	9	1 US-08-467-083-26
20	21	4	36.4	9	1 US-08-469-556A-27
21	22	4	36.4	9	1 US-08-414-417B-26
22	23	4	36.4	9	2 US-08-486-318A-26
23	24	4	36.4	9	2 US-08-734-591A-27
24	25	4	36.4	9	2 US-08-468-545B-26
25	26	4	36.4	9	2 US-08-169-660-27
26	27	4	36.4	9	3 US-08-396-385-12

Result No. Score Query Match Length DB ID Description

RESULT 1 US-09-056-105-33					
;	Sequence 33, Application US/09056105	;	Patent No. 6,387,569	;	GENERAL INFORMATION:
;	Applicant: KIPPS, THOMAS J.	;	Applicant: WU, YUNQI	;	Applicant: YUNQI
;	Title: VACCINES WITH ENHANCED INTRACELLULAR	;	Title: VACCINES WITH ENHANCED INTRACELLULAR	;	Title of Invention: VACCINES WITH ENHANCED INTRACELLULAR
;	;	;	;	;	;
;	File Reference: 233/231	;	File Reference: 233/231	;	File Reference: 233/231
;	Current Application Number: US/09/056,105	;	Current Application Number: US/09/056,105	;	Current Application Number: US/09/056,105
;	Current Filing Date: 1998-04-06	;	Earlier Application Number: 60/043,467	;	Current Filing Date: 1998-04-06
;	Earlier Application Date: 1997-04-10	;	Number of SEQ ID NOS: 35	;	Earlier Application Date: 1997-04-10
;	Software: FastSEQ for Windows Version 3.0	;	SEQ ID NO 33	;	Software: FastSEQ for Windows Version 3.0
;	Length: 11	;	Type: PRT	;	Length: 11
;	Organism: E.Coli	;	;	;	Organism: E.Coli
;	US-09-056-105-33	;	US-09-056-105-33	;	US-09-056-105-33

RESULT 2 US-09-425-585-1					
;	Sequence 1, Application US/09425585	;	Patent No. 6,348,315	;	GENERAL INFORMATION:
;	Applicant: PLUCKTHON, ANDREAS	;	Applicant: PLUCKTHON, ANDREAS	;	Applicant: PLUCKTHON, ANDREAS
;	Title: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES	;	Title of Invention: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES	;	Title of Invention: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
;	File Reference: PLUCK/1	;	File Reference: PLUCK/1	;	File Reference: PLUCK/1
;	Current Application Number: US/09/425,585	;	Current Application Number: US/09/425,585	;	Current Application Number: US/09/425,585
;	Current Filing Date: 1998-10-22	;	Current Filing Date: 1998-10-22	;	Current Filing Date: 1998-10-22
;	Prior Application Number: PCT/EP98/02420	;	Prior Application Number: PCT/EP98/02420	;	Prior Application Number: PCT/EP98/02420
;	Prior Filing Date: 1998-04-23	;	Prior Filing Date: 1998-04-23	;	Prior Filing Date: 1998-04-23
;	Number of SEQ ID NOS: 15	;	Number of SEQ ID NOS: 15	;	Number of SEQ ID NOS: 15
;	Software: PatentIn Ver. 2.1	;	Software: PatentIn Ver. 2.1	;	Software: PatentIn Ver. 2.1
;	SEQ ID NO 1	;	SEQ ID NO 1	;	SEQ ID NO 1
;	Length: 11	;	Length: 11	;	Length: 11
;	Type: PRT	;	Type: PRT	;	Type: PRT

Search Notes

ORGANISM: Escherichia coli
US-09-425-585-1

Query Match Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYAA 11
Db 1 AANDENYAA 11

RESULT 3
US-09-953-322-1

Sequence 1 Application US/09953321
Patent No. 6589741

GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: HAVNES, JOZEF
APPLICANT: JERMUTUS, LUTZ
TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
FILE REFERENCE: PLUCK/1 CON2
CURRENT APPLICATION NUMBER: US/09/953,321
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 09/425,585
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Escherichia coli
US-09-953-322-1

Query Match Score 11; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYAA 11
Db 1 AANDENYAA 11

RESULT 4
US-08-756-416-1

Sequence 1 Application US/08756416
Patent No. 6699715

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden, Martha
APPLICANT: Fell, Perry
APPLICANT: Mittler, Robert
APPLICANT: Winberg, Gosta
TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica, Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/756,416
FILING DATE: 27-NOV-1996

CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/007,755
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE DOCKET NUMBER: 30436.41US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
TELEK:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-756-416-1

Query Match Score 11; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYAA 11
Db 1 AANDENYAA 11

RESULT 5
US-09-443-501A-1

Sequence 1 Application US/09443501A
Patent No. 6303342

GENERAL INFORMATION:
APPLICANT: Kosan Biosciences, Inc.
APPLICANT: Julian, Bryan
APPLICANT: Katz, Leonard
APPLICANT: Khosla, Chaitan
APPLICANT: Tang, Li
APPLICANT: Ziermann, Rainer
TITLE OF INVENTION: Recombinant Methods and Materials for Producing
TITLE OF INVENTION: Epothilone and Epothilone Derivatives
FILE REFERENCE: 300662-20031.00
CURRENT APPLICATION NUMBER: US/09/443,501A
CURRENT FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: US 60/130,560
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/122,620
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: US 60/119,386
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: US 60/109,401
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ For Windows Version 4.0
SEQ ID NO 1
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-443-501A-1

Query Match Score 5; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YALAA 11
Db 14 YALAA 18

RESULT 6
US-08-484-905-85
Sequence 85, Application US/08484905
GENERAL INFORMATION:
Patent No. 5976551
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility Complex Determinant and Methods for Using the Complex (MHC) Determinant and Methods for Using the Complex (MHC)
TITLE OF INVENTION: Determinant and Methods for Using the Complex (MHC)
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/801,818
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 05-DEC-1991
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
PRIORITY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 85:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pocer, Jane B. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 14..15
OTHER INFORMATION: /note= "Xaa is an unidentified amino acid residue."
US-08-484-905-85

Query Match 45.5%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 85; Mismatches 0; Indels 0; Gaps 0;
Qy 6 NYALA 10
Db 8 NYALA 12

RESULT 8
US-08-370-476-85
Sequence 85, Application US/08370476
GENERAL INFORMATION:
Patent No. 6153408
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ocius, David
APPLICANT: Carrouge, Armand
TITLE OF INVENTION: Altered Major Histocompatibility Complex

RESULT 7
US-08-481-985B-85
Sequence 85, Application US/08481985B
GENERAL INFORMATION:
Patent No. 6011146
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre

ADDRESSEE: Dunner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/370,476
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/117,575
 FILING DATE: 07-SEP-1993
 APPLICATION NUMBER: US 08/072,787
 FILING DATE: 06-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/801,818
 FILING DATE: 05-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/792,473
 FILING DATE: 15-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 05243.0001-01000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEX/FAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 85:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Region
 LOCATION: 14..15
 OTHER INFORMATION: /note= "Xaa is an unidentified
 amino acid residue."
 US-08-370-476-85

Query Match 45.5%; Score 5; DB 3; Length 38;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAL 10
 Db 8 NYAL 12

RESULT 9
 US-09-493-795B-316
 Sequence 316, Application US/09493795B
 Patent No. 6797808

GENERAL INFORMATION:
 APPLICANT: Watkins, Maren
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Hillyard, David R.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Jones, Robert M.
 TITLE OF INVENTION: Alpha-Conotoxin Peptides
 FILE REFERENCE: 2314-179 A
 CURRENT APPLICATION NUMBER: US/09/493,795B
 CURRENT FILING DATE: 2000-01-28
 PRIOR APPLICATION NUMBER: US 60/118,381
 PRIOR FILING DATE: 1999-01-29
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 316

; LENGTH: 41 ;
; TYPE: PRT ;
; ORGANISM: Comus catus ;
; US-09-493-795B-316 ;
; Query Match 45.5%; Score 5; DB 4; Length 41;
; Best Local Similarity 100.0%; Pred. No. 91; Mismatches 0; Indels 0; Gaps 0;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 1 AANDE 5
; Db 7 AANDE 11

RESULT 10
 5217869-73
; Patent No. 5217869 ;
; APPLICANT: KAUVAR, LAWRENCE M. ;
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS ;
; NUMBER OF SEQUENCES: 121 ;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906 ;
; FILING DATE: 11-OCT-1988 ;
; SEQ ID NO:73 ;
; LENGTH: 5
; 5217869-73

Query Match 36.4%; Score 4; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAND 4
 Db 2 AAND 5

RESULT 11
 5227466-25
; Patent No. 5227466 ;
; APPLICANT: DEMEYTS, PIERRE ;
; TITLE OF INVENTION: INSULIN RECEPTOR BINDING SITE ;
; NUMBER OF SEQUENCES: 32 ;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/213,918 ;
; FILING DATE: 30-JUN-1988 ;
; SEQ ID NO:25 ;
; LENGTH: 5
; 5227466-25

Query Match 36.4%; Score 4; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAL 9
 Db 1 NYAL 4

RESULT 12
 5217869-73
; Patent No. 5217869 ;
; APPLICANT: KAUVAR, LAWRENCE M. ;
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS ;
; NUMBER OF SEQUENCES: 121 ;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906 ;
; FILING DATE: 11-OCT-1988 ;
; SEQ ID NO:73 ;
; LENGTH: 5
; 5217869-73

Query Match 36.4%; Score 4; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy: 1 AAND 4
 Db: 2 AAND 5

RESULT 13
 5227466-25
 ; Patent No. 5227466
 ; APPLICANT: DEMEYTS, PIERRE
 ; TITLE OF INVENTION: INSULIN RECEPTOR BINDING SITE
 ; NUMBER OF SEQUENCES: 32
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07-213,918
 ; FILING DATE: 30-JUN-1988
 ; SEQ ID NO: 25:
 ; LENGTH: 5

Query Match 36.4%; Score 4; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy: 6 NYAL 9
 Db: 1 NYAL 4

RESULT 14
 US-08-079-741A-101
 Sequence 101, Application US/08079741A
 ; Patent No. 5585275
 ; GENERAL INFORMATION:
 ; APPLICANT: SURNAME, OTHER NAMES and/or INITIALS
 ; APPLICANT: Johnson, Charles R.
 ; APPLICANT: Giebel, Lutz B.
 ; TITLE OF INVENTION: Pilot Apparatus For Peptide
 ; NUMBER OF SEQUENCES: 103
 ; CORRESPONDENCE ADDRESS: Inventors' Assignee's Counsel
 ; ADDRESSEE: ROSENBLUM, PARISH & ISAACS
 ; STREET: 160 W. Santa Clara Street, Suite 1500
 ; CITY: San Jose
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 95113

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte
 COMPUTER: IBM Clone
 OPERATING SYSTEM: MS-DOS 5.00
 SOFTWARE: WordPerfect 5.1, ASCII format (DOS text)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/079,741A
 FILING DATE: 18-JUNE-1993
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/939,065
 FILING DATE: 02-SEPT-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DULIN, JACQUES M.
 REGISTRATION NUMBER: 24, 067
 REFERENCE/DOCKET NUMBER: 5303-8

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (408) 977-0120
 TELEFAX: (408) 977-0129
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8
 TYPE: Amino Acids

STRANDEDNESS:
 TOPOLOGY: Linear
 MOLECULE TYPE: Peptide
 DESCRIPTION:
 NAME/KEY: Pepsyn-K Bead Test Peptide
 LOCATION:
 IDENTIFICATION METHOD: Constructed using a Milligen Biosearch Model 9600 peptide synthesizer.
 OTHER INFORMATION: Biological activity not determined.
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLISHING DATE:
 RELEVANT RESIDUES IN SEQ ID. NO: 101: From 1 to 8
 US-08-079-741A-101

Query Match 36.4%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy: 8 ALAA 11
 Db: 5 ALAA 8

RESULT 15
 US-07-939-065A-101
 Sequence 101, Application US/07939065A
 ; Patent No. 5591646
 ; GENERAL INFORMATION:
 ; APPLICANT: SURNAME, OTHER NAMES and/or INITIALS
 ; APPLICANT: Johnson, Charles R.
 ; APPLICANT: Giebel, Lutz B.
 ; TITLE OF INVENTION: Method and Apparatus For Peptide
 ; NUMBER OF INVENTION: Synthesis and Screening
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS: Inventor's/Assignee's Counsel
 ; ADDRESS: PILLSBURY MADISON & SUTRO
 ; STREET: Ten Almaden Boulevard, Suite 800
 ; CITY: San Jose
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 95113

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3-1/2 inch, 1.44M byte
 COMPUTER: IBM Clone
 OPERATING SYSTEM: MS-DOS 5.0
 SOFTWARE: WordPerfect 5.2, ASCII format (DOS text)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/939,065A
 FILING DATE: 02-Sept-1992
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NA
 ATTORNEY/AGENT INFORMATION:
 NAME: DULIN, JACQUES M.
 REGISTRATION NUMBER: 24, 067
 REFERENCE/DOCKET NUMBER: 5303-8

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (408) 947-4000
 TELEFAX: (408) 287-8341
 INFORMATION FOR SEQ ID NO: 101:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8
 TYPE: Amino Acids

LENGTH: 8
TYPE: Amino Acids
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
DESCRIPTION:
FEATURE:
NAME/KEY: Pepsyn-K Bead Test Peptide
LOCATION:
IDENTIFICATION METHOD: Constructed using a Milligen/Bioscanner Model 9600 peptide synthesizer.
IDENTIFICATION METHOD: Milligen/Bioscanner Model 9600 peptide synthesizer.
OTHER INFORMATION: Biological activity not determined. Xaa represents a random amino acid
OTHER INFORMATION: selected from mixtures of the following 10 amino acids to give equal incorporation: Nle, His, Pro, Gln, Tyr, Gly, Phe, Arg, Glu, Ala. Where Leu or Ala is specified at any position in the sequence, then Leu refers to Nle (or normal-leucine) and Ala refers to Ala (or beta-alanine).
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 101: 1 to 8
US-07-939-065A-101
Query Match Similarity 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 ALAA 11
| |||
Db 5 ALAA 8

Search completed: May 5, 2005, 18:24:18
Job time : 29 secs

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2005, 18:18:20 ; Search time 78 Seconds
(without alignments)

47.046 Million cell updates/sec

Title: US-10-827-133-9

Perfect score: 11

Sequence: 1 AANDENYALAA 11

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 1428581 seqs, 333598853 residues

Word size : 0

Total number of hits satisfying chosen parameters: 425092

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/ptodata/2/pubpaas/us07_PUBCOMB.pep:
 2: /cgn2_6/ptodata/2/pubpaas/fct_NEW_PUB.pep:
 3: /cgn2_6/ptodata/2/pubpaas/us06_NEW_PUB.pep:
 4: /cgn2_6/ptodata/2/pubpaas/us07_PUBCOMB.pep:
 5: /cgn2_6/ptodata/2/pubpaas/bctus_PUBCOMB.pep:
 6: /cgn2_6/ptodata/2/pubpaas/us07_NEW_PUB.pep:
 7: /cgn2_6/ptodata/2/pubpaas/us08_NEW_PUB.pep:
 8: /cgn2_6/ptodata/2/pubpaas/us08_PUBCOMB.pep:
 9: /cgn2_6/ptodata/2/pubpaas/us09A_PUBCOMB.pep:
 10: /cgn2_6/prodata/2/pubpaas/us09B_PUBCOMB.pep:
 11: /cgn2_6/prodata/2/pubpaas/us09C_PUBCOMB.pep:
 12: /cgn2_6/prodata/2/pubpaas/us09_NEW_PUB.pep:
 13: /cgn2_6/prodata/2/pubpaas/us10A_PUBCOMB.pep:
 14: /cgn2_6/prodata/2/pubpaas/us10B_PUBCOMB.pep:
 15: /cgn2_6/prodata/2/pubpaas/us10C_PUBCOMB.pep:
 16: /cgn2_6/prodata/2/pubpaas/us10D_PUBCOMB.pep:
 17: /cgn2_6/prodata/2/pubpaas/us10I_NEW_PUB.pep:
 18: /cgn2_6/prodata/2/pubpaas/us11A_NEW_PUB.pep:
 19: /cgn2_6/prodata/2/pubpaas/us60_NEW_PUB.pep:
 20: /cgn2_6/prodata/2/pubpaas/us60_PUBCOMB.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	9 US-09-953-321-1	Sequence 1, Appli
2	11	100.0	11	9 US-09-975-132A-3	Sequence 3, Appli
3	11	100.0	11	14 US-10-289-135A-119	Sequence 119, Appli
4	11	100.0	12	12 US-10-080-866-19	Sequence 19, Appli
5	6	54.5	6	14 US-10-037-243-3	Sequence 3, Appli
6	5	45.5	9	15 US-10-149-138-2806	Sequence 2806, Appli
7	5	45.5	9	15 US-10-149-138-1210	Sequence 4120, Appli
8	5	45.5	9	15 US-10-149-138-4153	Sequence 4153, Appli
9	5	45.5	9	16 US-10-149-138-2806	Sequence 2806, Appli
10	5	45.5	9	16 US-10-149-138-1210	Sequence 4120, Appli
11	5	45.5	9	16 US-10-149-138-4153	Sequence 4153, Appli
12	5	45.5	10	15 US-10-149-138-629	Sequence 629, Appli
13	5	45.5	10	15 US-10-149-138-2978	Sequence 2978, Appli

ALIGNMENTS

RESULT 1
US-09-953-321-1
 Sequence 1, Application US/09953321
 Patent No. US2010115083A1
 GENERAL INFORMATION:
 APPLICANT: PLUCKHUN, ANDREAS
 APPLICANT: HANES, JOZSEF
 APPLICANT: JERMOUTUS, LUTZ
 TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
 TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
 FILE REFERENCE: PLUCK1 CON2
 CURRENT APPLICATION NUMBER: US/09/953,321
 CURRENT FILING DATE: 2004-09-14
 PRIOR APPLICATION NUMBER: 09/425,585
 PRIOR FILING DATE: 1999-10-22
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 1
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Escherichia coli
 US-09-953-321-1

RESULT 2
US-09-975-132A-3
 Sequence 3, Application US/09975132A
 Publication No. US20020182672A1

GENERAL INFORMATION:
; APPLICANT: Kolkman, Marc
; TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by a Microorganism
; FILE REFERENCE: GCG616-2
; CURRENT APPLICATION NUMBER: US/09/975,132A
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/239,531
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide tag

Query Match Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00014; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Insertions 0; Gaps 0;

RESULT 5
US-10-080-866-19
; Sequence 11, Application US/10037243
; Publication No. US2003012435241
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates, LLC.
; ATTORNEY: Freimuth, Paul I
; ATTORNEY: Zhang, Yian-Biao
; ATTORNEY: Howitt, Jason A
; TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext
; CURRENT APPLICATION NUMBER: US/10/037,243
; FILE REFERENCE: BSA 01-22
; CURRENT FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic recognition motif
US-10-037-243-3

Query Match Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Insertions 0; Gaps 0;

RESULT 6
US-10-149-138-2806
; Sequence 6, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fixes, John
; ATTORNEY: Sette, Alessandro
; ATTORNEY: Sidney, John
; ATTORNEY: Southwood, Scott
; ATTORNEY: Chesnut, Robert
; ATTORNEY: Celiis, Esteban
; ATTORNEY: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060-0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299

RESULT 4
US-10-080-866-19
; Sequence 19, Application US/10080866
; Publication No. US20030109024A1
; GENERAL INFORMATION:
; APPLICANT: Paegle, E. Sasha
; APPLICANT: Reilly, Dorothea
; APPLICANT: Yansura, Daniel G.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1732RL
; CURRENT APPLICATION NUMBER: US 10/080,866

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; PRIORITY FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2806
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4153

Query Match          45.5%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db      6 NYALA 10
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Db      5 NYALA 9

RESULT 7
US-10-149-138-4120
; Sequence 4120, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060_0140001
; CURRENT APPLICATION NUMBER: US/10/149.138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-4120

Query Match          45.5%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db      6 NYALA 10
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Db      4 NYALA 8

RESULT 8
US-10-149-138-4153
; Sequence 4153, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060_0140001
; CURRENT APPLICATION NUMBER: US/10/149.138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2806
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2806

Query Match          45.5%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db      6 NYALA 10
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Db      5 NYALA 9

RESULT 10
US-10-149-138-4120
; Sequence 4120, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060_0140001
; CURRENT APPLICATION NUMBER: US/10/149.138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2806
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-2806

```

RESULT 12
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Ceis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060_0140001
; CURRENT APPLICATION NUMBER: US/10/149_138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591.
; PRIOR FILING DATE: 2000-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
; US-10-149-138-4120

Query Match 45.5%; Score 5; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 4 NYALA 8

RESULT 11
; Sequence 4153, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Ceis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060_0140001
; CURRENT APPLICATION NUMBER: PCT/US00/33591
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/10/149_138
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US/09/458_299
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4153
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
; US-10-149-138-4153

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Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 5 NYALA 9

RESULT 13
; Sequence 2978, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Ceis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060_0140001
; CURRENT APPLICATION NUMBER: PCT/US00/33591
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US/09/458_299
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2978
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptide
; US-10-149-138-2978

Query Match 45.5%; Score 5; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 6 NYALA 10

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Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Organism: Artificial Sequence
FEATURE: OTHER INFORMATION: Artificial Peptide
US-10-149-138-4411

RESULT 14
Qy 6 NYALA 10
Db 6 NYALA 10

RESULT 14
Qy 6 NYALA 10
Db 6 NYALA 10

Search completed: May 5, 2005, 18:31:04
Job time : 79 secs

TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: HBR2/neu Using Peptide and Nucleic Acid Compositions
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4331
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Artificial Peptide
US-10-149-138-4431

RESULT 15
Qy 6 NYALA 10
Db 6 NYALA 10

RESULT 15
Qy 6 NYALA 10
Db 6 NYALA 10

Search completed: May 5, 2005, 18:31:04
Job time : 79 secs

TITLE OF INVENTION: Inducing Cellular Immune Responses to
FILE REFERENCE: HBR2/neu Using Peptide and Nucleic Acid Compositions
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 4411
LENGTH: 10

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	Q8sha4 brookesia b	Q8sha4 brookesia b
OM protein - protein search, using SW model		Q8bk10 furcifer ca	Q8bk10 furcifer ca
Run on: May 5, 2005, 18:01:24 ; Search time: 92.3333 Seconds (without alignment)	61.006 Million cell updates/sec	Q708g1 ovis aries	Q708g1 ovis aries
Title: US-10-827-133-9	Perfect score: 11	Q93lx3 vibrio chol	Q93lx3 vibrio chol
Sequence: 1 AANDENYALAA 11	Scoring table: OLIGO	P80472 amycolatops	P80472 amycolatops
GapPop 60.0 , Gapext 60.0	Searched: 1612378 seqs, 512079187 residues	Q9bm22 euperipatoides	Q9bm22 euperipatoides
Word size : 0	Total number of hits satisfying chosen parameters: 68540	Q9bm24 leptofoxa x	Q9bm24 leptofoxa x
Minimum DB seq length: 0	Maximum DB seq length: 50	Q6d80 lepidomodium	Q6d80 lepidomodium
Post-processing: Listing first 45 summaries	Database : UniProt 03: 1: uniprot_sprot: 2: uniprot_trembl: *	Q7rg41 plasmoidium	Q7rg41 plasmoidium
		Q9gu44 scyphac raph	Q9gu44 scyphac raph
		Q9gu45 cypha raph	Q9gu45 cypha raph
		Q31210 mus musculus	Q31210 mus musculus
		Q700r9 sorghum bicolor	Q700r9 sorghum bicolor
		Q66269 cucumber mosquitofish	Q66269 cucumber mosquitofish
ALIGNMENTS			
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Q9UC79 PRELIMINARY; PRT: 26 AA.			
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	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)	
	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DB Interleukin-2 high-molecular-weight form (fragment).	
	OS Homo sapiens (Human)	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthesia; Primates; Cattarrhini; Hominidae; Homo.	
	OC NCBITaxID:9606;	OX NCBI_TaxID:9606;	
	RN [1]	RN RP	
SEQUENCE.			
RX MEDLINE=9217316; PubMed=7702741; PMID=7702741			
RA Ahmad Z., Ciolek D., Pan Y.C., Michel H., Khan F.R.; RT "purification and characterization of a high-molecular-weight form of recombinant human interleukin-2."			
RT J. Protein Chem. 13:591-598(1994).			
RL HSSP; P60568; IRL.			
DR GO:0005576; C:extracellular; IEA.			
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.			
DR GO; GO:0006955; F:immune response; IEA.			
DR InterPro; IPR0000779; Interleukin-2.			
DR Pfam; PF00715; IL2; 1.			
SQ SEQUENCE 26 AA; 2887 MW; 5B76899229356ED CRC64;			
Query Match 100.0%; Score 11; DB 2; Length 26;			
Best Local Similarity 100.0%; Pred. No. 0.00035; Mismatches 0; Indels 0; Gaps 0;			
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db 16 AANDENYALAA 26			
RESULT 2			
P96306 PRELIMINARY; PRT: 10 AA.			
ID P96306	AC P96306	DT 01-MAY-1997 (TREMBLrel. 03, Created)	
	DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)	DT 01-MAY-1998 (TREMBLrel. 08, Last annotation update)	
	DB Coded portion of proteolytic tag (fragment).	DB Coded portion of proteolytic tag (fragment).	
	OS Aeromonas salmonicida.	OS Aeromonas salmonicida.	
	OC Bacteria; Gammaproteobacteria; Aeromonadales; Aeromonadaceae; Aeromonas.	OC Bacteria; Gammaproteobacteria; Aeromonadales; Aeromonadaceae; Aeromonas.	
	OX NCBITaxID:645;	OX NCBITaxID:645;	
	RN SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	
RC STRAIN=ATCC 31658;			
RX MEDLINE=97128184; PubMed=8972778;			
RA Williams K.P., Barcel D.P.;			
RT "Phylogenetic analysis of tmRNA secondary structure.";			
Scoring table: OLIGO			
GapPop 60.0 , Gapext 60.0			
Searched: 1612378 seqs, 512079187 residues			
Word size : 0			
Total number of hits satisfying chosen parameters: 68540			
Minimum DB seq length: 0			
Maximum DB seq length: 50			
Post-processing: Listing first 45 summaries			
Database : UniProt 03: 1: uniprot_sprot: 2: uniprot_trembl: *			
1: uniprot_sprot: 2: uniprot_trembl: *			
*			
Result No. Score Match Length DB ID Description			
1 11 100.0 26 2 Q9UC79	Q9uc79 homo sapien		
2 10 90.9 10 2 P96306	P96306 aeromonas s		
3 10 90.9 10 2 P96321	P96321 escherichia		
4 10 90.9 10 2 P96352	P96352 marinobacter		
5 10 90.9 10 2 Q93LE5	Q93LE5 photobacter		
6 6 54.5 9 2 Q92LB4	Q93LE4 heliobacter		
7 6 54.5 10 2 P96423	P96423 pseudomonas		
8 5 45.5 10 2 P96421	P96421 neisseria g		
9 5 45.5 14 2 P96350	P96350 legionella		
10 5 45.5 35 2 Q96KJ8	Q96KJ8 sus scrofa		
11 5 45.5 49 2 Q8CKU9	Q8CKU9 yersinia pe		
12 5 45.5 50 1 HOXB ECOLI	P77091 escherichia		
13 4 36.4 8 2 Q62528	Q62528 mus spreatus		
14 4 36.4 12 2 Q7YKC3	Q7YKC3 ribes nevadensis		
15 4 36.4 13 2 Q7m355	Q7m355 ovis aries		
16 4 36.4 14 1 NAST_VESSEL	P01514 vespa lewisi		
17 4 36.4 15 2 Q9TwT5	Q9twt5 lumbicus t		
18 4 36.4 15 2 Q9TQQ5	Q9tqq5 bos taurus		
19 4 36.4 15 2 Q93LB6	Q93lb6 chloroflexu		
20 4 36.4 17 2 Q8k407	Q8k407 rattus norvegicus		
21 4 36.4 18 2 O06514	O06514 escherichia		
22 4 36.4 19 2 Q9MN29	Q9mn2 rattus norvegicus		
23 4 36.4 19 2 Q9PST5	Q9pst5 xenopus laevis		
24 4 36.4 20 2 Q15989	Q15989 homo sapiens		
25 4 36.4 20 2 Q9R4D9	Q9r4d9 escherichia		
26 4 36.4 21 2 Q9TRA9	Q9tra9 bos taurus		
27 4 36.4 21 2 QBVIL1	Q8vill1 mus musculus		
28 4 36.4 22 2 Q85513	Q85513 chlamydia t		
29 4 36.4 22 2 Q85515	Q85515 chlamydia t		
30 4 36.4 24 2 Q8SH95	Q8sh95 brookesia p		
31 4 36.4 24 2 Q8SH98	Q8sh98 brookesia p		

RL	RNA 2:1306-1310(1996).						
DR	EMBL; U68075; AAB48022; 1; -.						
FT	NON TER 1						
SQ	SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;						
	Query Match 90.9%; Score 10; DB 2; Length 10;						
	Best Local Similarity 100.0%; Pred. No. 0.0016;						
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	2 ANDENYALAA 11						
Db	1 ANDENYALAA 10						
	RESULT 5						
P96321	PRELIMINARY;	PRT;	10 AA.				
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AC	01-MAY-1997 (TREMBLrel. 03, Created)						
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)						
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)						
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OS	Bacillus coli.						
OC	Proteobacteria; Gammaproteobacteria; Vibrionales;						
OC	Enterobacteriales; Escherichia.						
NCBI_TaxID	562;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
STRAIN	=UTCC 133;						
RX	MEDLINE=9128184; PubMed=892778;						
RA	Williams K.P.; Bartel D.P.;						
RT	"Phylogenetic analysis of tRNA secondary structure.";						
RN	2:1306-1310(1996).						
[2]							
RP	SEQUENCE FROM N.A.						
RC	STRAIN=ATCC 133;						
RX	MEDLINE=9502883; PubMed=7524073;						
RA	Konine Y., Kitabatake M., Yokogawa T., Nishikawa K., Inokuchi H.;						
RT	"A tRNA-like structure is present in 10S RNA, a small stable RNA from Escherichia coli."						
RT	Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).						
RL	EMBL; U68074; AAB48024.1; -.						
DR	NON TER 1						
FT	SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;						
SQ	Query Match 90.9%; Score 10; DB 2; Length 10;						
	Best Local Similarity 100.0%; Pred. No. 0.0016;						
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	2 ANDENYALAA 11						
Db	1 ANDENYALAA 10						
	RESULT 6						
P96321	PRELIMINARY;	PRT;	9 AA.				
ID	Q93LE4;						
AC	01-MAY-1997 (TREMBLrel. 03, Created)						
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)						
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
DE	Coded portion of Proteolysis tag (Fragment).						
OS	Helicobacter hydrocarponicola (Peudomonas nautica).						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;						
OC	Alteromonadaceae; Marinobacter.						
NCBI_TaxID	2743;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=ATCC 49840.						
RX	MEDLINE=9128184; PubMed=892778;						
RA	Williams K.P.; Bartel D.P.;						
RT	"Phylogenetic analysis of tRNA secondary structure.";						
RL	RNA 2:1306-1310(1996).						
	SEQUENCE 9 AA; 937 MW; 7CD8D72DCB544AAB CRC64;						
	Query Match 90.9%; Score 10; DB 2; Length 10;						
	Best Local Similarity 100.0%; Pred. No. 0.0016;						
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	2 ANDENYALAA 11						
Db	1 ANDENYALAA 10						
	RESULT 7						
P96352	PRELIMINARY;	PRT;	10 AA.				
ID	P96352;						
AC	01-MAY-1997 (TREMBLrel. 03, Created)						
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)						
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
DE	Coded portion of Proteolysis tag (Fragment).						
OS	Marinobacter hydrocarponicola (Peudomonas nautica).						
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;						
OC	Alteromonadaceae; Marinobacter.						
NCBI_TaxID	2743;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=ATCC 49840.						
RX	MEDLINE=9128184; PubMed=892778;						
RA	Williams K.P.; Bartel D.P.;						
RT	"Phylogenetic analysis of tRNA secondary structure.";						
RL	RNA 2:1306-1310(1996).						
	SEQUENCE 9 AA; 937 MW; 7CD8D72DCB544AAB CRC64;						
	Query Match 90.9%; Score 10; DB 2; Length 10;						
	Best Local Similarity 100.0%; Pred. No. 0.0016;						
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	2 ANDENYALAA 11						
Db	1 ANDENYALAA 10						
	RESULT 8						
P96352	PRELIMINARY;	PRT;	10 AA.				
ID	P96352;						
AC	01-MAY-1997 (TREMBLrel. 03, Created)						
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)						
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)						
DE	Coded portion of Proteolysis tag (Fragment).						
OS	Helicobacter mobilis						
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteraceae;						
OC	Helicobacter.						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=ATCC 49840.						
RX	MEDLINE=9128184; PubMed=892778;						
RA	Williams K.P.; Bartel D.P.;						
RT	"The tRNA website.";						
RL	Nucleic Acids Res. 28:168-168 (2000).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=ATCC 200347;						
RX	MEDLINE=200347; PubMed=10592213; DOI=10.1093/nar/28.1.168;						
RA	Williams K.P.; Bartel D.P.;						
RT	"The tRNA website.";						
RL	Nucleic Acids Res. 28:168-168 (2000).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=ATCC 200347;						
RX	MEDLINE=200347; PubMed=10592213; DOI=10.1093/nar/28.1.168;						
RA	Williams K.P.; Bartel D.P.;						
RT	"The tRNA website.";						
RL	Nucleic Acids Res. 28:168-168 (2000).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=ATCC 200347;						
RX	MEDLINE=200347; PubMed=10592213; DOI=10.1093/nar/28.1.168;						
RA	Williams K.P.; Bartel D.P.;						
RT	"The tRNA website.";						
RL	Nucleic Acids Res. 28:168-168 (2000).						
RN	[2]						

Query Match Score 6; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALAA 11
Db 4 NYALAA 9

RESULT 7

P96423 PRELIMINARY; PRT; 10 AA.

ID P96423; Q7DCH6;
AC P96423; Q7DCH6;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Coded portion of proteolysis tag (Translated portion of tmRNA gene
ssrA) (Fragment).
GN OrderedLocusName=PA0826.1;
OS Pseudomonas aeruginosa;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

SEQUENCE FROM N.A.
STRAIN=ATCC 25320;
RC MEDLINE=9712818; PubMed=972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).

RN [2]

SEQUENCE FROM N.A.
STRAIN=ATCC 15632 / PA01;
RC MEDLINE=204373337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hufnagle W.O., Kowalik D.J., Lagrou M.,
Brinkman F.S.L., Hynes R.L., Tolentino E., Westbroek-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong Z., Paulsen I.T.,
Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.,
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
Nature 406:959-964(2000);
EMBL; U68078; AAB48059.1; -.
DR EMBL; AE004517; AA042616.1; -.
KW Complete proteome.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1037 MW; 857BD22DCB544AAA CRC64;

Query Match Score 6; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALAA 11
Db 5 NYALAA 10

RESULT 8

P96421 PRELIMINARY; PRT; 10 AA.

ID P96421; P96421;
AC P96421; P96421;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=ATCC 119424;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996);
EMBL; U68080; AAB48028.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1038 MW; 857BD22DCB41ABA1A CRC64;

Query Match Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YALAA 11
Db 6 YALAA 10

RESULT 9

P96350 PRELIMINARY; PRT;
ID P96350; P96350;
AC P96350;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DB Coded portion of proteolysis tag (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=ATCC 33152;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996);
EMBL; U68079; AAB48026.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1349 MW; CE5FF7318D8BE7D7D CRC64;

Query Match Score 5; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDEN 6
Db 1 ANDEN 5

RESULT 10

P9GK28 PRELIMINARY; PRT;
ID P9GK28; P9GK28;
AC P9GK28;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Apolipoprotein D (Fragment).
GN Name=APOD;
OS Sus scrofa (Pig).
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9833;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=21419000; PubMed=11528129;
RX MEDLINE=21419000; PubMed=11528129;
RA Van Poucke M., Yerle M., Tuggie C., Piumi F., Genet C.,
RA Van Zeerden A., Peelman L.J.;
RT "Integration of porcine chromosome 13 maps.";
RL CytoGenet. Cell Genet. 93:297-303(2001).
DR DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR011038; Calycin.
 DR InterPro; IPR000566; Lipocalin; 1.
 DR Pfam; Pfam0061; Lipocalin; 1.
 KW Lipoprotein.
 FT NON-TER 1 1
 FT NON-TER 35 35
 SQ SEQUENCE 35 AA; 4176 MW; EAA72C366D1C4AF1 CRC64;
 Query Match 45.5%; Score 5; DB 2; Length 35;
 Best Local Similarity 100.0%; Prod. No. 5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ENTYL 9
 |||||
 DB 4 ENTYL 8

RESULT 11
 Q8CKU9 PRELIMINARY; PRT; 49 AA.
 ID Q8CKU9
 AC Q8CKU9
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN Orderedlocusname=y2833;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Yersinia.
 RN [1] _TaxID=632;

RP SEQUENCE FROM N.A.
 RC STRAIN=KIM / Biorar Mediae realis;
 RX MEDLINE=22137863; PubMed=1242430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland K., Plunkett G. III, Boutin A., Mayhew G.P., Liss P.,
 Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 Fetherston J.D., Lindler L.E., Brubaker R.R., Piana G.V.,
 Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AB013886; AM86384.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 49 AA; 5616 MW; 8D8372953C8B7079 CRC64;
 Query Match 45.5%; Score 5; DB 2; Length 49;
 Best Local Similarity 100.0%; Prod. No. 6.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YALAA 11
 |||||
 DB 36 YALAA 40

RESULT 12
 HOKE_ECOLI STANDARD; PRT; 50 AA.
 ID HOKE_ECOLI_Q9R777;
 AC P77091; Q9R777;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1999 (Rel. 36, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE HOKE protein.
 GN Name=holsB; OrderedLocusName=b0561.1; ORFNames=h4415;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
 RN _TaxID=562;

RP SEQUENCE FROM N.A.
 RC STRAIN=X12 / MG1652;
 RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.,
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
 RA Komp C., Kurti O., Lew H., Lin D.,
 RA Federspiel N., Hyman R., Kalman S.,
 RA Namath A., Oefner P., Roberts D., Schramm S.,
 RA Submitted (JAN-1997) to the EMBL/GenBank/DDJB databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPTRAIN_X12;
 RX MEDLINE=97081202; PubMed=89052322;
 RA Ohshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Kajihara M., Kanai T., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiiuchi T.,
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155 (1996).
 RN [4]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE=99291074; PubMed=10361310;
 RA Pedersen K., Gerdes K.,
 RT "Multiple hok genes on the chromosome of Escherichia coli."
 RL Mol. Microbiol. 32:1090-1102 (1999)
 CC -|- SIMILARITY: Belongs to the hok/gef family.

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CC DR U00096; AA48122.1;
 DR EMBL; U82598; AAB40780.1; ALT_INIT.
 DR EMBL; D90700; BAA35222.1; ALT_INIT.
 DR EchoBase; BB4049;
 DR Ecogene; FG143.02; hokE.
 DR InterPro; IPR00021; Hok/gef_toxin.
 DR PF01848; HOK_GEF; 1.
 DR PRINTS; PR00281; HOKGEFTOXIC.
 DR Prodrom; PD005979; Hok/gef_toxin; 1.
 DR PROSITE; PS00556; HOK_GEF; 1.
 KW Complete proteome; Transmembrane.
 FT TRANSMEM 5 25 Potential.
 SQ SEQUENCE 50 AA; 5564 MW; 8AD9A981A6D46835 CRC64;

Query Match 45.5%; Score 5; DB 1; Length 50;
 Best Local Similarity 100.0%; Prod. No. 6.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YALAA 11
 |||||
 DB 5 YALAA 9

RESULT 13
 Q62528 PRELIMINARY; PRT; 8 AA.
 ID Q62528;
 AC Q62528;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

NCBI_TaxID=562;

[1]

RP SEQUENCE FROM N.A.
 RC STRAIN=X12 / MG1652;
 RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10096;
 RN [1] SEQUENCE FROM N.A.

RP STRAIN=SPPET/El;
 RC MEDLINE=941319082; PubMed=8043949;
 RX RA Nadeau J.H.; Wang X.; Horton J.H.; Hagen M.D.; Takahashi N.; Maezaki Y.;
 RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
 RL EMBL; U05632; AAB60463.1; -.
 PIR; I48935; I48935.
 KW Lipoprotein.
 FT NON TER 1 1
 SQ SEQUENCE 8 AA; 827 MW; 223DDDD72DC7633B CRC64;

Query Match 36.4%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 ALAA 11
 Db 4 ALAA 7

RESULT 14

Q7YKC3 PRELIMINARY; PRT; 12 AA.
 ID Q7YKC3
 AC Q7YKC3;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DB Photosystem Q (B) protein (Fragment).
 GN Name=pSBA;
 OS Ribes nevadense.
 OG Chloroplast.
 OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 OC Saxifragales; Grossulariaceae; Ribes.
 NCBI_TaxID=175221;
 RN [1]
 RP SEQUENCE FROM N.A.

RT "Molecular phylogeny and biogeography of *Ribes* (Grossulariaceae), with
 RT an emphasis on gooseberries (subg. *Grossularia*).";
 RL Syst. Bot. 29:77-96 (2004).
 DR EMBL; AY138090; AAP9245.1;
 DR GO; GO:000507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 1 1
 SQ SEQUENCE 12 AA; 110 MW; D6210A99A26DDDB02 CRC64;

Query Match 36.4%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 ALAA 11
 Db 1 ALAA 4

RESULT 15

Q7M355 PRELIMINARY; PRT; 13 AA.
 ID Q7M355
 AC Q7M355;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DB Glutathione peroxidase (EC 1.11.1.9) (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruminantia; Pecora; Bovidae;
 OC Mammalia; Buteraria; Cetartiodactyla; Ruminantia; Caprinae; Ovis.

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=9940;
 RN [1] SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.
 RX MEDLINE=92231574; PubMed=1567207;
 RA Gettins P.; Dyal D.; Crews B.;
 RT "Selenium-dependent glutathione peroxidases from ovine and bovine erythrocytes occur as longer chain forms than previously recognized.";
 RL Arch. Biochem. Biophys. 294:511-518(1992).
 DR PIR; A38923; A38929.

Query Match 36.4%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 ALAA 11
 Db 4 ALAA 7

Search completed: May 5, 2005, 18:22:50
 Job time : 94.3333 secs

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(USPTO)

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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:00:34 ; Search time: 101.333 Seconds
(without alignments)

Title: US-10-827-133-9

Perfect score: 11

Sequence: 1 AANDNTVALAA 11

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	AAB84403	Abb84403 E. coli d
2	11	100.0	11	AAO16101	Aao16101 C-terminal
3	11	100.0	11	ADB48279	Ad48279 TAT depen
4	11	100.0	11	ADF50155	Adf50155 S. enteri
5	11	100.0	12	AAE28994	Aae28994 Peptide u
6	6	54.5	6	ADU33753	Adl33753 Bacteriop
7	6	54.5	32	AAB61562	Aab61562 Peptide W
8	6	54.5	32	AAB61569	Aab61569 Peptide W
9	6	54.5	32	AAB61568	Aab61568 Peptide W
10	6	54.5	32	AAB61559	Aab61559 Peptide W
11	6	54.5	37	AAB61571	Aab61571 Peptide W
12	5	45.5	9	AGG88621	Aag88621 HER2/NEU
13	5	45.5	9	AGG88687	Aag88687 HER2/NEU
14	5	45.5	9	AAE31119	Aae31119 Human erb
15	5	45.5	9	ADN64564	Adn64564 HLA bindi
16	5	45.5	9	ADP80193	Adp80193 Human HLA
17	5	45.5	10	AAW70073	Aaw70073 HER-2/neu
18	5	45.5	10	AAY47715	Aay47715 Immunogen
19	5	45.5	10	AGG88761	Aag88761 HER2/NEU
20	5	45.5	10	AAU95886	Aau95886 Immunogen
21	5	45.5	10	ADN64603	Adn64603 HLA bindi
22	5	45.5	10	ADP80218	Adp80218 Human HLA
23	5	45.5	14	AAY98935	Aay98935 HLA Class
24	5	45.5	15	AAR48500	Aar48500 Histobran
25	5	45.5	15	AAR48506	Aar48506 Histobran

ALIGNMENTS

RESULT 1
ID ABB84403 standard; peptide; 11 AA.
XX ABB84403;
XX DT 21-OCT-2002 (first entry)
XX DE E. coli derived aberrant protein C-terminal peptide motif.
XX KW Tumour antigen; murine; vaccine; cellular immune response; immunogen; cancer; tumour.
XX OS Escherichia coli.
XX PN US6287569-B1.
XX PD 11-SEP-2001.
XX PF 06-APR-1998; 98US-00056105.
XX PR 10-APR-1997; 97US-0043467P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Kipps TJ, Wu Y;
XX DR WPI ; 1998-583198/49.
XX PT Generating cellular immune response in patient to target protein - comprises introducing vector with nucleotide sequence encoding immunogen comprising protein processing signal into cell of patient.
XX PT Example 5 ; Col 6; 61pp; English.

This invention describes a novel method for generating a cellular immune response in a patient to a target protein or its fragment. The method involves introducing a vector containing a nucleotide sequence encoding a chimeric immunogen comprising a protein processing signal and the target protein or its fragment. The immunogen is produced by the cells and processed so that the target protein or its fragment is presented to the patients immune system and a cellular immune response is initiated. The method and vectors can be used as a form of vaccination and could be used to generate a cellular immune response in patients to, e.g. dangerous tumours. The cellular immune response is the predominant immune response in the patient. This sequence represents an E. coli aberrant protein motif used in the method of the invention. Note: The information in this spec has been previously disclosed in WO199845444 however this spec

CC contained no sequence information
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AANDENYALAA 11
 Db 1 AANDENYALAA 11
 OS Synthetic.
 XX PN WO2003040335-A2.

RESULT 2
 AAC16101
 ID AAO16101 standard; peptide; 11 AA.
 XX AAO16101;
 AC AAO16101;
 XX 27-FEB-2003 (first entry)
 DT 27-FEB-2003 (first entry)
 XX C-terminal tag peptide.
 KW Gene therapy; vaccine; humoral immune response; cellular immune response;
 KW immune response modulation; pathogenic infection; rheumatoid arthritis.
 XX Unidentified.
 OS WO20028181-A1.
 PN WO20028181-A1.
 XX 24-OCT-2002.
 PD 24-OCT-2002.
 XX 18-APR-2002; 2002WO-AU000486.
 PR 18-APR-2001; 2001AU-00004468.
 PA (UTQU) UNIV QUEENSLAND.
 XX Frazer LH;
 PT 2003-075509/07.
 New compositions having antigens, polynucleotides encoding the antigens,
 or antigen-presenting cells, useful for modulating an immune response,
 e.g., for treating or preventing pathogenic infections or rheumatoid
 arthritis.
 XX Disclosure; Page 35; 139pp; English.
 XX The invention comprises compositions for eliciting a humoral or cellular
 immune response against a target antigen. The compositions of the
 invention are useful for eliciting a humoral and cellular immune response
 against a target antigen, modulating an immune response in a patient, and
 the treatment or prophylaxis of a disease or condition. This includes
 pathogenic infections (e.g. viral, bacterial, fungal or protozoan), or an
 immune response to an autoantigen (e.g. rheumatoid arthritis). The
 present amino acid sequence represents a peptide which was used in the
 invention
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 11; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AANDENYALAA 11
 Db 1 AANDENYALAA 11
 OS Synthetic.
 XX PN WO2003040335-A2.

RESULT 3
 ADE48279 standard; peptide; 11 AA.
 ID ADE48279

XX AC ADB48279;
 XX DT 29-JAN-2004 (first entry)
 DE TAT dependant secretion clone #1.
 XX KW leader peptide; Twin Arginine Translocation pathway;
 KW putative TAT leader peptide sequence.
 XX OS Synthetic.
 XX PN WO2003040335-A2.
 PD 15-MAY-2003.
 XX PF 05-NOV-2002; 2002WO-US035618.
 XX PR 05-NOV-2001; 2001US-0337452P.
 XX PR 21-AUG-2002; 2002US-0337452P.
 PA (RERE-) RES DEV FOUND.
 XX PI Georgian G, Delisa M;
 XX DR WPI; 2003-449453/42.
 XX PR Identifying a leader peptide that directs increased protein export in
 bacteria by screening libraries of leader peptides for sequences that
 allow rapid export and can rescue short-lived reporter protein from
 degradation in cytoplasm.
 XX PR Example 7; SEQ ID NO 119; 63pp; English.
 XX PR The present sequence relates to identifying a leader peptide that directs
 increased protein export in bacteria, optionally through the Twin
 Arginine Translocation pathway, comprises screening of libraries of
 putative leader peptides or their mutants for sequences that allow rapid
 export and, thus, can rescue a short-lived reporter protein from
 degradation in the cytoplasm. The method is useful in engineering of
 leader peptides for the secretion of recombinant proteins in bacteria.
 CC The leader peptides can be used to direct or enhance protein secretion.
 CC The present sequence represents a putative TAT leader peptide sequence of
 the invention.
 XX SQ Sequence 11 AA;
 CC Query Match 100.0%; Score 11; DB 7; Length 11;
 CC Best Local Similarity 100.0%; Pred. No. 0.00018;
 CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AANDENYALAA 11
 Db 1 AANDENYALAA 11
 DE S. enteritidis protease C-terminal fragment.
 XX KW promoter; mutant; vaccine; Shine Dalgarno; probiotic bacteria;
 KW regulatory gene; targeted optimisation.
 XX OS Salmonella enteritidis.
 XX PN WO2003040335-A2.

XX (UZYU-) UNIV ZUERICH.
 PA
 XX Plueckthun A, Arndt K, Mueller K, Pelletier J;
 PI
 XX WPI: 2001-137954/14.
 DR
 XX PT Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.
 XX PS Claim 6; Page 41; 56pp; English.
 CC The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention
 XX SQ Sequence 32 AA;

Query Match 54.5%; Score 6; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DENYAL 9
 Db 13 DENYAL 18

RESULT 11
 AAB6171
 ID AAB61571 standard; peptide; 37 AA.
 DE Peptide WINZIPB1 used to identify hetero-associating peptides.
 KW Hetero-associating coiled-coil peptide; heterodimerisation.
 XX DT 03-APR-2001 (first entry)
 XX DB Peptide WinZip-B1 used to identify hetero-associating peptides.
 XX KW Hetero-associating coiled-coil peptide; heterodimerisation.
 XX AC AAB61571;
 XX DT 03-APR-2001 (first entry)
 XX DB Peptide WinZip-B1 used to identify hetero-associating peptides.
 XX KW Hetero-associating coiled-coil peptide; heterodimerisation.
 XX AC AAB61571;
 XX FT 37 /note= "C-terminal amide"
 XX FT 37 /note= "N-terminal acetyl"
 XX FH 1 Location/Qualifiers
 XX FT Key Modified-Site
 XX FT Modified-Site
 XX FT Modified-Site
 XX FT Modified-Site
 XX PN WO200100814-A2.
 XX PD 04-JAN-2001.
 XX PF 26-JUN-2000; 2000WO-EP005922.
 XX PR 25-JUN-1999; 99US-00344096.
 XX PA (UZYU-) UNIV ZUERICH.
 XX PI Plueckthun A, Arndt K, Mueller K, Pelletier J;
 XX DR 2001-137954/14.
 XX WPI; 2001-137954/14.
 XX PT Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.
 XX PS Example 3; Page 27; 56pp; English.
 XX CC The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for
 CC via a screenable or selectable property caused by the hetero-association
 CC of the two peptides. The identified peptides can be used for
 CC heterodimerisation of fusion proteins. The present sequence is a hetero-
 CC associating peptide that can be used in method of the present invention
 XX SQ Sequence 37 AA;

Query Match 54.5%; Score 6; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DENYAL 9

XX (UZYU-) UNIV ZUERICH.
 PA
 XX Plueckthun A, Arndt K, Mueller K, Pelletier J;
 PI
 XX WPI: 2001-137954/14.
 DR
 XX PT Identifying heteroassociating (poly)peptides involves designing an
 PT appropriate coiled-coil library and screening by using a library versus
 PT library approach.
 XX PS Claim 6; Page 40; 56pp; English.
 CC The present invention relates to a method for identifying hetero-
 CC associating coiled-coil peptides. The method comprises providing a
 CC library of peptides with the general formula of AAB61546, and a second
 CC library of peptides with the general formula of AAB61547. Hetero-
 CC association of peptides from the two libraries can then be screened for

Db		Qy	6 NYALA 10
	16 DENTAL 21	Db	4 NYALA 8
RESULT 12		RESULT 13	
AAG88621		AAG88627	standard; peptide; 9 AA.
ID AAG88621		ID AAG88627	standard; peptide; 9 AA.
AC AAG88621;		XX	
XX	11-SEP-2001 (first entry)	AC	
DT		XX	
XX	HER2/NEU DR supermotif binding peptide core sequence #167.	DT	11-SEP-2001 (first entry)
DE		XX	
XX	HUMAN; HER2/neu; epitope; human leukocyte antigen; HLA; T cell; immune response; vaccine; tumour; cancer; cytotoxic; immunostimulant; tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL; OS Homo sapiens.	DE	HER2/NEU DR 3a motif binding peptide core sequence #112.
OS		XX	
OS	WO00141787-A1.	XX	
PN		PN	
XX	14-JUN-2001.	XX	
PD		PD	
XX	11-DEC-2000; 2000WO-US033591.	XX	
PR		PP	11-DEC-2000; 2000WO-US033591.
XX	10-DEC-1999; 99US-00458299.	XX	
PA	(EPMI-) EPIMMUNE INC.	PR	10-DEC-1999; 99US-00458299.
XX		XX	
PI	Fikes J., Sette A., Sidney J., Southwood S., Chesnut R., Celis E.; Keogh E.;	PA	(EPMI-) EPIMMUNE INC.
XX		PI	
DR	WPI; 2001-374995/39.	Keogh E;	
XX		XX	
PT	An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer.	DR	WPI; 2001-374995/39.
PT		PT	An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer.
PS	Disclosure; Page 172; 199pp; English.	PT	An isolated prepared HER2/neu epitope useful in a vaccine for inducing cellular immune responses for the prevention and treatment of cancer.
XX		PS	Disclosure; Page 174; 199pp; English.
CC	The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vitro and binds to a complex of an epitope (I), bound to a human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (III) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding peptide comprising (I) and (5) an isolated nucleic acid encoding (III). (1) has cytotoxic and immunostimulant activities and can be used in vaccines. (I), (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (III) are useful for monitoring or evaluating an immune response to a tumour-associated antigen when incubated with a T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour-tumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG89126 to AAG89121 represent amino acid sequences used in the exemplification of the present invention.	XX	The present invention describes isolated prepared HER2/neu epitopes (I). Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vitro and binds to a complex of an epitope (I), bound to a human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I) and a second epitope and the peptide is less than 50 contiguous amino acids that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (III) comprising (II) and a pharmaceutical excipient; (4) an isolated nucleic acid encoding a peptide comprising (I) and (5) an isolated nucleic acid encoding (III). (I) has cytotoxic and immunostimulant activities and can be used in vaccines. (I), (II) and (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (III) are useful for monitoring or evaluating an immune response to a tumour-associated antigen when incubated with a T lymphocyte sample form a patient and detecting the presence of bound T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour-tumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG89126 to AAG89121 represent amino acid sequences used in the exemplification of the present invention.
SQ	Sequence 9 AA;	XX	Sequence 9 AA;
Query Match	45.5%; Score 5; DB 4; Length 9;	XX	Query Match
Best Local Similarity	100.0%; Pred. No. 1.8e+06;	XX	Best Local Similarity
Matches 5	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	Matches 5
		XX	Score 5; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; HLA binding peptide #1164.

Qy 6 NYALA 10
Db 5 NYALA 9

RESULT 14
ID AAE31119 Standard; peptide: 9 AA.
XX AAE31119;
AC AAB31119;
DP 24-FEB-2003 (first entry)
XX Human erb2 peptide #4.
XX Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
XX Homo sapiens.
PN WO200272627-A2.
XX 19-SEP-2002.
XX 11-MAR-2002; 2002WO-EP002666.
PR 09-MAR-2001; 2001US-0274250P.
PR 14-MAY-2001; 2001US-0290333P.
PR 18-MAY-2001; 2001US-0291610P.
PA (CALL-) CALLISTOGEN AG.

PI Wrede P, Walden P, Eichler-Mertens M, Filter M;
DR WPI: 2002-759836-82.

PT Providing, identifying or optimizing peptides for inducing cytotoxic T-lymphocytes and for treating cancer, comprises selecting conserved regions in antigenic proteins and identifying CD8+ T-cell epitopes in the protein.

PS Disclosure; Page 7: 32pp; English.

XX The invention relates to a method for providing, identifying or and optimising peptides which induce cytotoxic T-lymphocytes and to the uses of the obtained peptides for vaccination. The method is useful for providing, identifying and/or optimising peptides that are useful in manufacturing a pharmaceutical composition for the induction of cytotoxic T-lymphocytes, and for the prevention, treatment or diagnosis of cancer or viral infections. The invention is also used in gene therapy. The present sequence is human erb2 peptide used to illustrate the method of the invention.

SQ Sequence 9 AA;

Query Match Score 5; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 5 NYALA 9

RESULT 15
ADN64564
ID ADN64564 Standard; peptide: 9 AA.
XX ADN64564;
AC ADN64564;
XX 01-JUL-2004 (first entry)

Query Match Score 5; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYALA 10
Db 5 NYALA 9

Search completed: May 5, 2005, 18:18:05
Job time : 102.333 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	30	4	36.4	45	2	A05163
OM protein - protein search, using bw model	Gene ac protein - recombinant prot	31	4	36.4	46	1	ACBPT4
Run on: May 5, 2005, 18:10:34 ; Search time 20.3333 Seconds (without alignments)	34K epidermal grow hypothetical prote	32	4	36.4	47	2	A56778
Title: US-10-827-133-9	protein C inhibitio	33	4	36.4	48	2	A56771
Perfect score: 11	T-cell receptor al	34	4	36.4	48	2	A54368
Sequence: 1 AANDENYALAA 11	hypothetical prote	35	4	36.4	48	2	S59076
Scoring table: OLIGO	protein	36	4	36.4	49	2	BX0029
Gapop 60.0 , Gapext 60.0	R-Phycocerythrin ga	37	4	36.4	49	2	A34530
Searched: 283416 seqs, 96216763 residues	callifMRFAamide 8 -	38	4	36.4	50	2	D69287
Word size : 0	hypothetical prote	39	4	36.4	50	2	C82690
Total number of hits satisfying chosen parameters: 11837	thyroglobulin - do	40	3	27.3	54	2	S18401
Minimum DB seq length: 0	zinc-binding prote	41	3	27.3	5	2	S55237
Maximum DB seq length: 50	19 heavy chain CRD	42	3	27.3	5	2	PR0281
Post-processing: Listing first 45 summaries	trM protein - bac	43	3	27.3	5	2	A32014
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	R-Phycocerythrin ga	44	3	27.3	8	2	A37521
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	callifMRFAamide 8 -	45	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	hypothetical prote	46	3	27.3	8	2	H41978
Minimum DB seq length: 0	thyroglobulin - do	47	3	27.3	8	2	H41978
Maximum DB seq length: 50	zinc-binding prote	48	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	19 heavy chain CRD	49	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	trM protein - bac	50	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	R-Phycocerythrin ga	51	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	callifMRFAamide 8 -	52	3	27.3	8	2	H41978
Minimum DB seq length: 0	hypothetical prote	53	3	27.3	8	2	H41978
Maximum DB seq length: 50	thyroglobulin - do	54	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	zinc-binding prote	55	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	19 heavy chain CRD	56	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	trM protein - bac	57	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	R-Phycocerythrin ga	58	3	27.3	8	2	H41978
Minimum DB seq length: 0	callifMRFAamide 8 -	59	3	27.3	8	2	H41978
Maximum DB seq length: 50	hypothetical prote	60	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	thyroglobulin - do	61	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	zinc-binding prote	62	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	19 heavy chain CRD	63	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	trM protein - bac	64	3	27.3	8	2	H41978
Minimum DB seq length: 0	R-Phycocerythrin ga	65	3	27.3	8	2	H41978
Maximum DB seq length: 50	callifMRFAamide 8 -	66	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	hypothetical prote	67	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	thyroglobulin - do	68	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	zinc-binding prote	69	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	19 heavy chain CRD	70	3	27.3	8	2	H41978
Minimum DB seq length: 0	trM protein - bac	71	3	27.3	8	2	H41978
Maximum DB seq length: 50	R-Phycocerythrin ga	72	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	callifMRFAamide 8 -	73	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	hypothetical prote	74	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	thyroglobulin - do	75	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	zinc-binding prote	76	3	27.3	8	2	H41978
Minimum DB seq length: 0	19 heavy chain CRD	77	3	27.3	8	2	H41978
Maximum DB seq length: 50	trM protein - bac	78	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	R-Phycocerythrin ga	79	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	callifMRFAamide 8 -	80	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	hypothetical prote	81	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	thyroglobulin - do	82	3	27.3	8	2	H41978
Minimum DB seq length: 0	zinc-binding prote	83	3	27.3	8	2	H41978
Maximum DB seq length: 50	19 heavy chain CRD	84	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	trM protein - bac	85	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	R-Phycocerythrin ga	86	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	callifMRFAamide 8 -	87	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	hypothetical prote	88	3	27.3	8	2	H41978
Minimum DB seq length: 0	thyroglobulin - do	89	3	27.3	8	2	H41978
Maximum DB seq length: 50	zinc-binding prote	90	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	19 heavy chain CRD	91	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	trM protein - bac	92	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	R-Phycocerythrin ga	93	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	callifMRFAamide 8 -	94	3	27.3	8	2	H41978
Minimum DB seq length: 0	hypothetical prote	95	3	27.3	8	2	H41978
Maximum DB seq length: 50	thyroglobulin - do	96	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	zinc-binding prote	97	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	19 heavy chain CRD	98	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	trM protein - bac	99	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	R-Phycocerythrin ga	100	3	27.3	8	2	H41978
Minimum DB seq length: 0	callifMRFAamide 8 -	101	3	27.3	8	2	H41978
Maximum DB seq length: 50	hypothetical prote	102	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	thyroglobulin - do	103	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	zinc-binding prote	104	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	19 heavy chain CRD	105	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	trM protein - bac	106	3	27.3	8	2	H41978
Minimum DB seq length: 0	R-Phycocerythrin ga	107	3	27.3	8	2	H41978
Maximum DB seq length: 50	callifMRFAamide 8 -	108	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	hypothetical prote	109	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	thyroglobulin - do	110	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	zinc-binding prote	111	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	19 heavy chain CRD	112	3	27.3	8	2	H41978
Minimum DB seq length: 0	trM protein - bac	113	3	27.3	8	2	H41978
Maximum DB seq length: 50	R-Phycocerythrin ga	114	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	callifMRFAamide 8 -	115	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	hypothetical prote	116	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	thyroglobulin - do	117	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	zinc-binding prote	118	3	27.3	8	2	H41978
Minimum DB seq length: 0	19 heavy chain CRD	119	3	27.3	8	2	H41978
Maximum DB seq length: 50	trM protein - bac	120	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	R-Phycocerythrin ga	121	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	callifMRFAamide 8 -	122	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	hypothetical prote	123	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	thyroglobulin - do	124	3	27.3	8	2	H41978
Minimum DB seq length: 0	zinc-binding prote	125	3	27.3	8	2	H41978
Maximum DB seq length: 50	19 heavy chain CRD	126	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	trM protein - bac	127	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	R-Phycocerythrin ga	128	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	callifMRFAamide 8 -	129	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	hypothetical prote	130	3	27.3	8	2	H41978
Minimum DB seq length: 0	thyroglobulin - do	131	3	27.3	8	2	H41978
Maximum DB seq length: 50	zinc-binding prote	132	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	19 heavy chain CRD	133	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	trM protein - bac	134	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	R-Phycocerythrin ga	135	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	callifMRFAamide 8 -	136	3	27.3	8	2	H41978
Minimum DB seq length: 0	hypothetical prote	137	3	27.3	8	2	H41978
Maximum DB seq length: 50	thyroglobulin - do	138	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	zinc-binding prote	139	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	19 heavy chain CRD	140	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	trM protein - bac	141	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	R-Phycocerythrin ga	142	3	27.3	8	2	H41978
Minimum DB seq length: 0	callifMRFAamide 8 -	143	3	27.3	8	2	H41978
Maximum DB seq length: 50	hypothetical prote	144	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	thyroglobulin - do	145	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	zinc-binding prote	146	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	19 heavy chain CRD	147	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	trM protein - bac	148	3	27.3	8	2	H41978
Minimum DB seq length: 0	R-Phycocerythrin ga	149	3	27.3	8	2	H41978
Maximum DB seq length: 50	callifMRFAamide 8 -	150	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	hypothetical prote	151	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	thyroglobulin - do	152	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	zinc-binding prote	153	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	19 heavy chain CRD	154	3	27.3	8	2	H41978
Minimum DB seq length: 0	trM protein - bac	155	3	27.3	8	2	H41978
Maximum DB seq length: 50	R-Phycocerythrin ga	156	3	27.3	8	2	H41978
Post-processing: Listing first 45 summaries	callifMRFAamide 8 -	157	3	27.3	8	2	H41978
Database : PIR 7.9: 1: pir1: 2: pir2: 3: pir3: 4: pir4: 5:	hypothetical prote	158	3	27.3	8	2	H41978
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	thyroglobulin - do	159	3	27.3	8	2	H41978
Total number of hits satisfying chosen parameters: 11837	zinc-binding prote	160	3	27.3	8	2	H41978
Minimum DB seq length: 0	19 heavy chain CRD	161	3	27.3			

S11298 hemagglutinin precursor - influenza A virus (strain A/E/PV/Rostock/34 [H7N1]) (fragment)
 C;Species: Influenza A virus
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 08-Apr-1994
 C;Accession: S11298
 R;Robertson,
 J.S.
 Nucleic Acids Res. 6, 3745-3757, 1979
 A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza
 A;Reference number: S11286; MUID:80034428; PMID:493121

Query Match Score 4; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 DB 5 ALAA 8

RESULT 6

A46586 hemoglobin (N-terminal, linker chain L2) - earthworm (Lumbricus terrestris) (fragment)
 C;Species: Lumbricus terrestris (common earthworm)
 C;Accession: A46586
 C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 R;Ownby, D.W.; Zhu, H.; Schneider, K.; Beavis, R.C.; Chait, B.T.; Riggs, A.F.
 R;Owby, D.W.; Zhu, H.; Schneider, K.; Beavis, R.C.; Chait, B.T.; Riggs, A.F.
 A;Title: The extracellular hemoglobin of the earthworm, *Lumbricus terrestris*. Determination
 A;Reference number: A46586; MUID:93293879; PMID:8514787

A;Accession: A46586
 A;Status: preliminary
 A;Molecule type: protein
 A;Cross-references: UNIPROT:Q97WTS
 A;Note: sequence extracted from NCBI backbone (NCBIP:134509)

Query Match Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 DB 9 ALAA 12

RESULT 7

A3929 glutathione Peroxidase (EC 1.11.1.9) - sheep (fragment)
 C;Species: Ovis orientalis aries,Ovis aries (domestic sheep)
 C;Accession: A3929
 C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 R;Betterns, P.; Dyal, D.; Crews, B.
 Arch. Biochim. Biophys. 294, 511-518, 1992
 A;Title: Selenium-dependent glutathione peroxidases from ovine and bovine erythrocytes
 A;Reference number: S21712; MUID:92231574; PMID:1567207

Query Match Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 DB 4 ALAA 7

RESULT 8

S19616 polychaete (*Budistylia vancouveri*) (fragment)
 N;Alternate names: chlorocrorin
 C;Species: Budistylia vancouveri
 C;Accession: S19616
 C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 R;Oabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H.
 J. Mol. Biol. 222, 1109-1129, 1991
 A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular chl
 A;Reference number: S19532; MUID:92106333; PMID:1765147

OmegaVAV mastoparan - yellowjacket (*Vespa lewisi*)
 C;Species: *Vespa lewisi*
 C;Accession: A01776
 R;Hirai, Y.; Yasuhara, T.; Yoshiida, H.; Nakajima, T.; Fujino, M.; Kitada, C.
 Chem. Pharm. Bull. 27, 1942-1944, 1979
 A;Title: A new mast cell degranulating peptide mastoparan in the venom of *Vespa-lewisi*
 A;Reference number: A01776; MUID:80155337; PMID:540362

Query Match Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ALAA 11
 DB 12 ALAA 15

RESULT 5

A;Cross-references: UNIPROT:P01514
 A;Residues: 1-14 <H1R>
 A;Molecule type: protein
 A;Accession: A01776
 A;Cross-references: UNIPROT:P01514
 A;Residues: 1-14 <H1R>
 A;Molecule type: protein
 A;Accession: A01776
 A;Cross-references: This coacoactive peptide was also synthesized
 A;Comment: This coacoactive peptide from wasp venom induces mast cell degranulation. The
 C;Superfamily: mastoparan
 C;Keywords: amidated carboxyl end
 F;14/Modified site: amidated carboxyl end (Leu) #status experimental

A; Accession: S19616
 A; Molecule type: protein
 A; Residues: 1-20 <QAB>
 C; Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dodeca
 C; Keywords: calcium; dodecamer; hemotetramer; oxygen carrier

Query Match 36.4%; Score 4; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YALA 10
 Db ||||| 10 YALA 13

RESULT 9
 A47209 histone H-1-MDBP-2 - chicken (fragments)
 C;Species: Gallus gallus (chicken)
 C;Accession: A47209
 R;Jost, J.P.; Hoisteng, J.
 Proc. Natl. Acad. Sci. U.S.A. 89, 9499-9503, 1992
 A;Title: The repressor MDBP-2 is a member of the histone H1 family that binds preferentially to DNA
 A;Reference number: A47209; MUID:93028489; PMID:1409659
 A;Accession: A47209
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <J0JS>

Query Match 36.4%; Score 4; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ALAA 11
 Db ||||| 14 ALAA 17

RESULT 10
 A33210 protein disulfide-isomerase (EC 5.3.4.1), pancreatic - dog (fragment)
 N;Alternative names: S-S rearrangease
 C;Species: Canis lupus familiaris (dog)
 C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 12-Apr-1995
 R;Michalak, M.
 submitted to the Protein Sequence Database, July 1991
 A;Accession number: A33210
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-27 <MC>
 C;Superfamily: protein disulfide-isomerase; thioredoxin homology
 C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 36.4%; Score 4; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ALAA 11
 Db ||||| 20 ALAA 23

RESULT 11
 PC4234 hypothetical protein 27 - Synechococcus sp. (fragment)
 C;Species: Synechococcus sp.
 C;Accession: PC4234
 R;Fujishiro, T.; Kaneko, T.; Sugita, M.; Sugita, M.
 DNA Res. 3, 165-169, 1996

A;Title: Organization and transcription of a putative gene cluster encoding ribosomal proteins
 A;Reference number: JCS120; MUID:97061204; PMID:8905234
 A;Accession: PC4234
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-27 <FUJ>
 A;Cross-references: UNIPROT:Q55018; DDBJ:D85103
 A;Experimental source: strain PCC6301

Query Match 36.4%; Score 4; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ALAA 11
 Db ||||| 10 ALAA 13

RESULT 12
 T14210 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Uromastyx acanthinurus mitochondrial
 C;Species: mitochondrial Uromastyx acanthinurus
 C;Date: 20-Sep-1999 #text_change 20-Sep-1999 #sequence_revision 20-Sep-1999
 C;Accession: T14210
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Pang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997
 A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A;Reference number: Z17789; MUID:91104; PMID:9000757
 A;Accession: T14210
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-28 <MAC>
 A;Cross-references: UNIPROT:P92760; EMBL:U71325; NID:91753264; PID:91753265; PMID:AAC622
 A;Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology, Univers
 C;Genetics:
 A;Genome: mitochondrial
 A;Note: ND1
 C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[N1Fe]-hydrogenase-3-t
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 36.4%; Score 4; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ALAA 11
 Db ||||| 19 ALAA 22

RESULT 13
 E81239 hypothetical protein NMBA093 [Imported] - Neisseria meningitidis
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: E81239
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A., Hri, H.; Qin, H.; Vanathavat, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoport, R.; Ve
 A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A;Reference number: A81000; MUID:2017555; PMID:10710307
 A;Accession: E81239
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-28 <ET>
 A;Cross-references: UNIPROT:Q9KIL8; GB:AE002368; GB:AE002369; NID:AE002098; PMID:AAF4055
 A;Experimental source: serogroup B, strain MC58.
 C;Genetics:

Query Match 36.4%; Score 4; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;

	Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	3	NDEN 6								
Db	3	NDEN 6								

RESULT 14

139799
 CAV-66 - *Bacillus pumilus* (fragment)
 C;Species: *Bacillus pumilus*
 C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I39799
 R;Duvall, E.J.; Williams, D.M.; Mongkolsuk, S.; Lovett, P.S.
 J. Bacteriol. 158, 784-790, 1984
 A;Title: Regulatory regions that control expression of two chloramphenicol-inducible cat
 A;Reference number: 139799; PMID:84212298; PMID:6327638
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-30 <RETS>
 A;Cross-references: UNIPROT:Q45356; GB:K01811; NID:9142647; PID:AAA22292.1; PID:9551696
 C;Superfamily: chloramphenicol acetyltransferase

Query Match Score 4 ; DB 2 ; Length 30;
 Best Local Similarity 100.0% ; Pred. No. 7e+02;
 Matches 4 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

	Matches	4 DENY 7		Db	6 DENY 9
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RESULT 15

F60529
 heocyanin M1 - crayfish (*Cherax destructor*) (fragment)
 C;Species: *Cherax destructor* (yabby)
 C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 11-May-2000
 C;Accession: F60529
 R;Neuteboom, B.; Sierdema, S.J.; Beintema, J.J.
Comp. Biochem. Physiol. B 94, 587-592, 1989
 A;Title: The relationship between N-terminal sequences and immunological characterization
 A;Reference number: A60529; PMID:90151075; PMID:2620501
 A;Accession: F60529
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-32 <NEU>

Query Match Score 4 ; DB 2 ; Length 32;
 Best Local Similarity 100.0% ; Pred. No. 7.5e+02;
 Matches 4 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

	Matches	3 NDEN 6		Db	27 NDEN 30
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Search completed: May 5, 2005, 18:25:30
 Job time : 22.3333 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
1	8	72.7	11	3	US-09-056-105-33		Sequence 33, Appl
2	8	72.7	11	3	US-09-025-585-1		Sequence 1, Appl
3	8.	72.7	11	4	US-09-953-321-1		Sequence 1, Appl
4	8	72.7	11	4	US-08-4156-416-1		Sequence 1, Appl
5	5	45.5	11	2	US-08-4179-611-14		Sequence 14, Appl
6	5	45.5	41	4	US-09-493-795B-316		Sequence 316, Appl
7	4	36.4	4	6	5215909-6		Patent No. 5215909
8	4	36.4	5	6	5217869-73		Patent No. 5217869
9	4	36.4	6	1	US-07-954-133-7		Sequence 7, Appl
10	4	36.4	5	6	5215909-6		Sequence 11, Appl
11	4	36.4	6	1	US-09-060-722A-11		Sequence 16, Appl
12	4	36.4	7	3	US-09-060-722A-11		Sequence 16, Appl
13	4	36.4	7	3	US-09-190-964-16		Sequence 11, Appl
14	4	36.4	7	4	US-09-845-849A-11		Sequence 48, Appl
15	4	36.4	8	3	US-08-588-988-48		Sequence 74, Appl
16	4	36.4	9	1	US-01-178-570-74		Sequence 74, Appl
17	4	36.4	9	3	US-08-369-64-74		Sequence 74, Appl
18	4	36.4	9	3	US-09-133-062D-17		Sequence 74, Appl
19	4	36.4	9	5	PCT-US95-00147-74		Sequence 169, Appl
20	4	36.4	10	1	US-08-218-022A-169		Sequence 8, Appl
21	4	36.4	10	2	US-08-518-967-8		Sequence 16, Appl
22	4	36.4	12	1	US-08-405-200-16		Sequence 5, Appl
23	4	36.4	12	3	US-08-536-257A-5		Sequence 5, Appl
24	4	36.4	12	3	US-08-860-339-5		Sequence 5, Appl
25	4	36.4	12	4	US-09-370-644B-5		Sequence 5, Appl
26	4	36.4	12	4	US-09-573-629-5		Sequence 5, Appl
27	4	36.4	12	4	US-10-208-349-5		Sequence 5, Appl

i ORGANISM: Escherichia coli
i US-09-425-585-1

Query Match 72.7%; Score 8; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; N mismatches 0; Indels 0;
Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8

RESULT 3
US-09-953-321-1
Sequence 1, Application US/09953321
Patent No. 6589741
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: HANES, JOZEF
APPLICANT: JEREMUTIS, LUTZ
TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEAR ACID MOLECULES ENCODING
FILE REFERENCE: PLUCK/1 CON2
CURRENT APPLICATION NUMBER: US/09/953, 321
CURRENT FILING DATE: 2001-09-14
PRIOR FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 11
TYPE: PRT
ORGANISM: Escherichia coli
US-09-953-321-1

Query Match 72.7%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; N mismatches 0; Indels 0;
Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8

RESULT 4
US-08-756-416-1
Sequence 1, Application US/08756416
Patent No. 6699715
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden, Marsha
APPLICANT: Felt, Perry
APPLICANT: Mittler, Gosta
APPLICANT: Winberg, Gosta
TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
TITLE OF INVENTION: MEDIATE ADHESION BETWEEN CELLS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica, Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756, 416
FILING DATE: 27-NOV-1996

CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/007, 755
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34, 470
REFERENCE/DOCKET NUMBER: 30436.41US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-756-416-1
Query Match 72.7%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 8; Conservative 0; N mismatches 0; Indels 0;
Gaps 0;
Qy 1 AANDENYA 8
Db 1 AANDENYA 8
RESULT 5
US-08-419-614-14
Sequence 14, Application US/08479614
Patent No. 5861294
GENERAL INFORMATION:
APPLICANT: Cowart, Marlon Daniel, Halbert, Donald N.,
APPLICANT: Kerwin, Jr., James F., McNally, Teresa
TITLE OF INVENTION: Adenosine Kinase Polypeptides
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: D-377 AP6D, 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: Macintosh System 7.1
OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479, 614
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32, 159
REFERENCE/DOCKET NUMBER: 5749.US.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4884
TELEFAX: (708) 938-2623
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

```

US-08-479-614-14
Query Match      45.5%; Score 5; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy    7 YAA SV 11
Db     4 YAA SV 8

RESULT 6
; Sequence 316, Application US/09493795B
; Patent No. 6797808
GENERAL INFORMATION
; APPLICANT: Watkins, Maren
; APPLICANT: Oliver, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Alpha-Conotoxin Peptides
FILE REFERENCE: 2314-179.A
CURRENT APPLICATION NUMBER: US/09/493,795B
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 404
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 316
LENGTH: 41
TYPE: PRT
ORGANISM: Conus catus
US-09-493-795B-316

Query Match      45.5%; Score 5; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy    1 AANDE 5
Db     1 AANDE 11

RESULT 7
5215909-6
; Patent No. 5215909
; APPLICANT: SOREQ, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO: 6:
; LENGTH: 4
5215909-6

Query Match      36.4%; Score 4; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy    8 AASV 11
Db     1 AASV 4

RESULT 8
5215909-6
Query Match      36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy    1 AAND 4
Db     2 AAND 5

RESULT 11
US-07-994-133-7

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Sequence 7, Application US/07994133
Patent No. 5436392
GENERAL INFORMATION:
; APPLICANT: Kanost, Michael R.
; APPLICANT: Bohnert, Hans J.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING M. SEXTA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
ZIP: 80303

COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,133
; FILING DATE: 1992/12/21
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenlee, Lorance L.
; REGISTRATION NUMBER: 27,894
; REFERENCE/DOCKET NUMBER: 48-92
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/499-8080
; TELEFAX: 303/499-8089
; TELEX: 823189
; INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-994-133-7

Query Match 36.4%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 1 AASV 4

RESULT 12
US-09-060-726A-11
; Sequence 11, Application US/09060726A
; Patent No. 6225530
GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS 026A
; CURRENT APPLICATION NUMBER: US/09/060,726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-060-726A-11

Query Match 36.4%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 1 AASV 4

RESULT 13
US-09-190-964-16
; Sequence 16, Application US/09190964
; Patent No. 6228989
GENERAL INFORMATION:
; APPLICANT: Traugh, Jolinda A.
; APPLICANT: Thazon, Polygena T.
; TITLE OF INVENTION: Peptide Substrates Phosphorylated By P21-Activated Protein Kinase
; FILE REFERENCE: 1229-276/988425
; CURRENT APPLICATION NUMBER: US/09/190,964
; CURRENT FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-190-964-16

Query Match 36.4%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 3 AASV 6

RESULT 14
US-09-845-849A-11
; Sequence 11, Application US/09845849A
; Patent No. 6713663
GENERAL INFORMATION:
; APPLICANT: WEIGEL, Detlef
; APPLICANT: KARDALUSKY, Igor
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS 026DV1
; CURRENT APPLICATION NUMBER: US/09/845,849A
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/060,726
; SEQ ID NO: 11
; LENGTH: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-845-849A-11

Query Match 36.4%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 1 AASV 4

RESULT 15
US-08-088-998-48
; Sequence 48, Application US/08688998B
; Patent No. 5436392
GENERAL INFORMATION:
; APPLICANT: Kanost, Michael R.
; APPLICANT: Bohnert, Hans J.
TITLE OF INVENTION: PROTEASE INHIBITOR
; FILE REFERENCE: SALKINS 026A
; CURRENT APPLICATION NUMBER: US/09/060,726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-060-726A-11

Query Match 36.4%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Patent No. 6096545
GENERAL INFORMATION
APPLICANT: Leebvre, Daniel D.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
FILE REFERENCE: PP96-03
CURRENT APPLICATION NUMBER: US/08/688,988B
NUMBER OF SEQ ID NOS: 48
SEQ ID NO 48
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 8
TYPE: PRT
ORGANISM: Arabidopsis Thaliana
US-08-688-988-48

Query Match 36.4%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ANDE 5
|||
Db 4 ANDE 7

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Job time : 29 secs

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OM protein - protein search, using sw model

Run.on: May 5, 2005, 18:18:20 ; Search time 78 Seconds (without alignments)

47.046 Million cell updates/sec

Title: US-10-827-133-10

Perfect score: 11

Sequence: 1 AANDENYAAVS 11

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Minimum DB seq length: 0

Maximum DB seq length: 50

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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
 US-09-953-321-1 ; Sequence 1, Application US/099533121 ; Patent No. US2002115083A1 ; GENERAL INFORMATION: ; APPLICANT: PLUCHTHUN, ANDREAS ; APPLICANT: HANES, JOSEF ; APPLICANT: JEROMUTS, LUTZ ; TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES ENCODING FILE REFERENCE: PLUCK/1 CON2 CURRENT APPLICATION NUMBER: US/09/953,321 ; CURRENT FILING DATE: 2001-09-14 ; PRIOR APPLICATION NUMBER: 09/425,585 ; PRIORITY FILING DATE: 1999-10-22 ; NUMBER OF SEQ ID NOS: 15 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 1 ; LENGTH: 11 ; TYPE: PRT ; ORGANISM: Escherichia coli ; US-09-953-321-1

Sequence 1, Appli
 Sequence 3, Appli
 Sequence 119, Appli
 Sequence 19, Appli
 Sequence 3, Appli
 Sequence 107, Appli
 Sequence 108, Appli
 Sequence 114, Appli
 Sequence 159, Appli
 Sequence 96, Appli
 Sequence 5, Appli
 Sequence 5, Appli
 Sequence 316, Appli

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	72.7	11	9 US-09-953-321-1	Sequence 1, Appli
2	8	72.7	11	9 US-09-975-122A-3	Sequence 3, Appli
3	8	72.7	11	14 US-10-289-135A-119	Sequence 119, Appli
4	8	72.7	12	14 US-10-080-066-19	Sequence 19, Appli
5	6	54.5	6	14 US-10-037-243-3	Sequence 3, Appli
6	5	45.5	16	14 US-10-031-874A-107	Sequence 107, Appli
7	5	45.5	16	14 US-10-031-874A-108	Sequence 108, Appli
8	5	45.5	17	14 US-10-031-874A-114	Sequence 114, Appli
9	5	45.5	17	14 US-10-031-874A-159	Sequence 159, Appli
10	5	45.5	19	19 US-09-977-197A-96	Sequence 96, Appli
11	5	45.5	19	14 US-10-026-925-5	Sequence 5, Appli
12	5	45.5	19	15 US-10-425-555-5	Sequence 5, Appli
13	5	45.5	41	17 US-10-895-372-316	Sequence 316, Appli

RESULT 2
 US-09-975-132A-3 ; Sequence 3, Application US/09975132A1 ; Publication No. US2002182672A1

GENERAL INFORMATION:
 ; APPLICANT: Kolkman, Marc
 ; TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by a Microorganism
 ; FILE REFERENCE: GCG6-6-2
 ; CURRENT APPLICATION NUMBER: US/09/975,132A
 ; CURRENT FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: US 60/239,531
 ; PRIOR FILING DATE: 2000-10-10
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic peptide tag
 ; US-09-975-132A-3

Query Match Score 72.7%; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.93; Indels 0; Gaps 0;

RESULT 3
 US-10-289-135A-119
 ; Sequence 119, Application US/10289135A
 ; Publication No. US200310180937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GEORGIU, GEORGE
 ; APPLICANT: DELISA, MATTHEW
 ; TITLE OF INVENTION: ENGINEERING OF LEADER PEPTIDES FOR THE SECRETION OF RECOMBINANT PROTEINS IN BACTERIA
 ; FILE REFERENCE: CLFR:019US
 ; CURRENT APPLICATION NUMBER: US/10/289,135A
 ; CURRENT FILING DATE: 2003-01-28
 ; PRIOR APPLICATION NUMBER: 60/337,452
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 134
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 119
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 ; US-10-289-135A-119

Query Match Score 72.7%; DB 14; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.093; Indels 0; Gaps 0;

RESULT 4
 US-10-080-866-19
 ; Sequence 19, Application US/10080866
 ; Publication No. US2003109024A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paegle, E. Sasha
 ; APPLICANT: Reilly, Dorotha
 ; APPLICANT: Yansura, Daniel G.
 ; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF POLYPEPTIDES
 ; CURRENT APPLICATION NUMBER: US/10/080,866

GENERAL INFORMATION:
 ; CURRENT FILING DATE: 2002-02-22
 ; PRIOR APPLICATION NUMBER: US 60/274,384
 ; PRIOR FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 19
 ; SEQ ID NO: 19
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide for generating antibodies
 ; US-10-080-866-19

Query Match Score 72.7%; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.1; Indels 0; Gaps 0;

RESULT 5
 US-10-037-243-3
 ; Sequence 3, Application US/10037243
 ; Publication No. US20030134352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brookhaven Science Associates, LLC.
 ; APPLICANT: Freimuth, Paul I
 ; APPLICANT: Zhang, Yian-Biao
 ; APPLICANT: Howitt, Jason A
 ; TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext
 ; CURRENT APPLICATION NUMBER: US/10/037,243
 ; FILE REFERENCE: BSA 01-22
 ; CURRENT FILING DATE: 2002-06-03
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 3
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic recognition motif
 ; US-10-037-243-3

Query Match Score 54.5%; DB 14; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;

RESULT 6
 US-10-031-874A-107
 ; Sequence 107, Application US/10031874A
 ; Publication No. US2003010598A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANHA, JAMSHID
 ; APPLICANT: DUBUC, GINETTE
 ; APPLICANT: NARANG, SARAN
 ; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS DERIVED FROM LLAMA ANTIBODIES
 ; FILE REFERENCE: 11054-1
 ; CURRENT APPLICATION NUMBER: US/10/031,874A
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/207,234
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 107
 ; LENGTH: 16
 ; TYPE: PRT


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APPLICANT: LADNER, ROBERT C. LIBRARIES OF GENETIC PACKAGES
TITLE OF INVENTION: FOCUSED LIBRARIES OF GENETIC PACKAGES
FILE REFERENCE: DYAX/004
CURRENT APPLICATION NUMBER: US/10/026,925
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 5
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Heavy chain
FEATURE: OTHER INFORMATION: CDR2 vector
FEATURE: NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Any amino acid except Cys
FEATURE: NAME/KEY: MOD_RES
LOCATION: (3)
OTHER INFORMATION: Any amino acid except Cys
FEATURE: NAME/KEY: MOD_RES
LOCATION: (5)..(7)
OTHER INFORMATION: Any amino acid except Cys
FEATURE: NAME/KEY: MOD_RES
LOCATION: (12)
OTHER INFORMATION: Any amino acid except Cys
US-10-026-925-5

Query Match Score 5; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 YAASV 11
Db 13 YAASV 17

RESULT 13
US-10-895-372-316
Sequence 316, Application US/10895372
Publication No. US20050032705A1
GENERAL INFORMATION:
APPLICANT: Watkins, Maren
APPLICANT: Olivera, Baldomero M.
APPLICANT: Hilliard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Jones, Robert M.
TITLE OF INVENTION: Alpha-Conotoxin Peptides
FILE REFERENCE: 2314-286
CURRENT APPLICATION NUMBER: US/10/895,372
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: US 09/493,795
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US/10/895,372
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 60/118,381
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 316
LENGTH: 41
TYPE: PRT
ORGANISM: Conus catus
US-10-895-372-316

Query Match Score 5; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AANDE 5
Db 7 AANDE 11

RESULT 14
US-10-424-599-211029
Sequence 211029, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(51223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 211029
LENGTH: 46
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_32586C.1.pep
US-10-424-599-211029

Query Match Score 5; DB 15; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 13 NYAS 17

RESULT 15
US-10-424-599-250324
Query Match Score 5; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 YAASV 11
Db 13 YAASV 17

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; Sequence 250324, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250324
; LENGTH: 8
; TYPE: PR
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_68070C.1.pep
; OTHER INFORMATION: US-10-424-399-250324

Query Match 45.5%; Score 5; DB 15; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 YAASV 11
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Db 38 YAASV 42

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	72.7	11	2 ABB84403	Aba16101 E. coli d C termina Ad48279 TAT depen Adf50155 S. enteri Aae28994 Peptid u Ad133153 Bacteriop Aaw08376 Rat brain Aaw73649 Rat adeno Aau82541 Llama CDR Aau82542 Llama CDR Aau82548 Llama CDR Aau82594 Llama CDR Abp62282 Human imm Aaw15584 Anti-RSV Aay05048
2	8	72.7	11	6 AAO16101	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
3	8	72.7	11	7 ADB48279	Adf50155 S. enteri Aae28994 Peptid u Ad133153 Bacteriop Aaw08376 Rat brain Aaw73649 Rat adeno Aau82541 Llama CDR Aau82542 Llama CDR Aau82548 Llama CDR Aau82594 Llama CDR Abp62282 Human imm Aaw15584 Anti-RSV Aay05048
4	8	72.7	11	7 ADF50155	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
5	6	54.5	6	7 ADL33753	Adf50155 S. enteri Aae28994 Peptid u Ad133153 Bacteriop Aaw08376 Rat brain Aaw73649 Rat adeno Aau82541 Llama CDR Aau82542 Llama CDR Aau82548 Llama CDR Aau82594 Llama CDR Abp62282 Human imm Aaw15584 Anti-RSV Aay05048
6	5	45.5	11	2 AAW08376	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
7	5	45.5	11	2 AAW08376	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
8	5	45.5	16	5 AAU82541	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
9	5	45.5	16	5 AAU82541	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
10	5	45.5	16	5 AAU82542	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
11	5	45.5	17	5 AAU82548	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
12	5	45.5	17	5 AAU82594	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
13	5	45.5	18	5 ABP62282	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
14	5	45.5	19	2 AAW16584	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
15	5	45.5	19	2 AAY05048	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
16	5	45.5	19	6 ABP56777	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
17	5	45.5	19	6 ADC82814	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
18	5	45.5	22	7 ADC33576	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
19	5	45.5	32	4 AAB61562	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
20	5	45.5	32	4 AAB61569	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
21	5	45.5	32	4 AAB61568	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
22	5	45.5	32	4 AAB61559	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
23	5	45.5	37	4 AAB61571	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
24	5	45.5	41	3 AAB21594	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo
25	5	45.5	49	2 AAY11212	Abp56777 Focused 1 Adc82814 CDR regio Adc33576 Fusion pe Abb61562 Peptide W Abb61569 Peptide W Abb61568 Peptide W Abb61566 Peptide W Abb61559 Peptide W Abb61571 Peptide W Abb21594 Cone snai Aay11212 S. pneumo

ALIGNMENTS

RESULT 1
 ABB84403
 ID ABB84403 standard; peptide; 11 AA.
 XX
 AC ABB84403;
 XX
 DT 21-OCT-2002 (first entry)

E. coli derived aberrant protein C-terminal peptide motif.
 DE
 XX
 KW Tumour antigen; murine; vaccine; cellular immune response; immunogen; cancer; tumour.
 XX
 OS Escherichia coli.
 XX
 US6287569-B1.
 PN
 XX
 PD 11-SEP-2001.
 XX
 PF 06-APR-1998;
 XX
 PR 10-APR-1997;
 XX
 XX
 (REGC) UNIV CALIFORNIA.
 PI Kipps TJ, Wu Y;
 XX
 DR WPI ; 1998-583198/49.

Generating cellular immune response in patient to target protein - comprising introducing vector with nucleotide sequence encoding immunogen comprising protein processing signal into cell of patient.

XX
 PR 10-APR-1997;
 XX
 XX
 97US-0043467P.
 XX
 XX
 Example 5; Col 6; 61pp; English.

This invention describes a novel method for generating a cellular immune response in a patient to target protein or its fragment. The method involves introducing a vector containing a nucleotide sequence encoding a chimeric immunogen comprising a protein processing signal and the target protein or its fragment. The immunogen is produced by the cells and processed so that the target protein or its fragment is presented to the patients immune system and a cellular immune response is initiated. The method and vectors can be used as a form of vaccination and could be used to generate a cellular immune response in patients to, e.g. cancerous tumours. The cellular immune response is the predominant immune response in the patient. This sequence represents an E. coli aberrant protein motif described in the method of the invention. Note: The information in this spec has been previously disclosed in WO199845444 however this spec

CC contained no sequence information
 XX Sequence 11 AA;

Query Match 72.7%; Score 8; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
 Db 1 AANDENYA 8

RESULT 2
 AAO16101 standard; peptide; 11 AA.
 ID AAO16101
 XX
 AC AAO16101;
 XX DT 27-FEB-2003 (first entry)
 XX
 DE C-terminal tag peptide.
 XX KW Gene therapy; vaccine; humoral immune response; cellular immune response; pathogenic infection; rheumatoid arthritis.
 XX
 OS Unidentified.
 XX WO200283181-A1.
 XX PD 24-OCT-2002.
 XX PF 18-APR-2002; 2002WO-AU000486.
 XX PR 18-APR-2001; 2001AU-00004468.
 XX PA (UYOU) UNIV QUEENSLAND.
 XX PI Fraser IH;
 XX DR WPI; 2003-075509/07.
 XX PT New compositions having antigens, polynucleotides encoding the antigens, or antigen-presenting cells, useful for modulating an immune response, e.g. for treating or preventing pathogenic infections or rheumatoïd arthritis.
 XX Disclosure; Page 35; 139pp; English.
 XX The invention comprises compositions for eliciting a humoral or cellular immune response against a target antigen. The compositions of the invention are useful for eliciting a humoral and cellular immune response against a target antigen, modulating an immune response in a patient, and the treatment or prophylaxis of a disease or condition. This includes pathogenic infections (e.g. viral, bacterial, fungal or protozoan), or an immune response to an autoantigen (e.g. rheumatoid arthritis). The present amino acid sequence represents a peptide which was used in the invention
 XX Sequence 11 AA;

XX XX XX DT 29-JAN-2004 (first entry)
 DE TAT dependant secretion clone #1.
 KW leader peptide; Twin Arginine Translocation pathway;
 XX putative TAT leader peptide sequence.
 OS Synthetic.
 XX PN WO2003040335-A2.
 XX PD 15-MAY-2003.
 XX PF 05-NOV-2002; 2002WO-US035618.
 XX PR 05-NOV-2001; 2001US-0337452P.
 XX PR 21-AUG-2002; 2002US-0337452P.
 XX PA (REBE-) RES DEV FOUND.

PI Georgiou G, Delisa M;
 XX DR WPI; 2003-449453/42.

XX Identifying a leader peptide that directs increased protein export in bacteria by screening libraries of leader peptides for sequences that allow rapid export and can rescue short-lived reporter protein from degradation in cytoplasm.

XX PS Example 7; SEQ ID NO 119; 63pp; English.

XX The present sequence relates to identifying a leader peptide that directs increased protein export in bacteria, optionally through the Twin Arginine Translocation pathway, comprises screening of libraries of putative leader peptides or their mutants for sequences that allow rapid export and, thus, can rescue a short-lived reporter protein from degradation in the cytoplasm. The method is useful in engineering of leader peptides for the secretion of recombinant proteins in bacteria. The leader peptides can be used to direct or enhance protein secretion. The present sequence represents a putative TAT leader peptide sequence of the invention.

XX SQ Sequence 11 AA;

Query Match 72.7%; Score 8; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
 Db 1 AANDENYA 8

RESULT 4
 ADF0155 standard; peptide; 11 AA.
 ID ADF0155
 XX AC ADF0155;
 XX DT 12-FEB-2004 (first entry)
 S. enteritidis protease C-terminal fragment.

XX KW promoter; mutant; vaccine; Shine Dalgarno; probiotic bacteria;
 XX regulatory gene; targeted optimisation.
 OS Salmonella enteritidis.
 PN WO2003070941-A2.

RESULT 3
 ADE48279 standard; peptide; 11 AA.
 ID ADE48279

PD 28-AUG-2003.
 XX DR WPI; 2002-723363/78.
 PP 19-FEB-2003; 2003WO-EP001676.
 XX PT New vector comprising anti-termination nucleic acid or RNA encoding the
 PR PT polypeptide with non-lambda promoter, useful for producing human
 PR PT thrombopoietin (TPO) or fibroblast growth factor-5 (FGF-5) polypeptide.
 XX PS Example 2; Page 32; 70pp; English.

XX The invention relates to vectors for producing a polypeptide heterologous
 PT to prokaryotic cells and method for producing the polypeptide. The method
 CC is useful for producing a polypeptide heterologous to prokaryotic cells.
 CC The present sequence is a peptide used in the exemplification of the
 CC invention

XX Sequence 12 AA;
 PS Query Match 72.7%; Score 8; DB 5; Length 12;
 XX Best Local Similarity 100.0%; Pred. No. 0.059;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AANDENYA 8
 Db 2 AANDENYA 9

RESULT 6
 CC ADL33753 standard; protein; 6 AA.
 CC ID ADL33753
 CC XX AC ADL33753;
 CC XX DT 20-MAY-2004 (first entry)
 CC DE Bacteriophage T7 ssrA peptide.
 CC KW protein solubility; coxsackievirus and adenovirus receptor; CAR;
 CC KW Bacteriophage T7; ssrA peptide.
 CC XX OS Enterobacteria phage T7.
 CC XX PN US2003134552-A1.
 CC XX PD 17-JUL-2003.
 CC XX PF 04-JAN-2002; 2002US-00037243.
 CC XX PR 04-JAN-2002; 2002US-00037243.

XX Sequence 11 AA;
 PS Query Match 72.7%; Score 8; DB 7; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AANDENYA 8
 Db 1 AANDENYA 8

RESULT 5
 AAE28994 standard; peptide; 12 AA.
 ID AAE28994
 AC AAE28994;
 XX DT 27-JAN-2003 (first entry)
 XX DB Peptide used in the exemplification of the invention.
 XX KW Vector; prokaryotic cell.
 XX OS Unidentified.
 PN WO200372847-A2.
 XX PD 19-SEP-2002.
 XX PF 22-FEB-2002; 2002WO-US005069.
 XX PR 09-MAR-2001; 2001US-0274384P.
 PA (GETH) GENENTECH INC.
 PA Paegle ES, Reilly D, Yansura DG;

XX The invention relates to a method of enhancing the solubility of, and
 CC promoting the adoption of native protein conformation of a recombinantly
 CC expressed polypeptide by expressing the polypeptide as a fusion protein
 CC including a peptide extension with: net negative charge (not peptide T7A)
 CC positioned at the carboxyl terminus; or net charge +2 to -20, positioned
 CC at the amino terminus. The nucleic acids encoding the polypeptide of
 CC interest and the extension are fused and inserted into an expression
 CC vector which is then introduced into a host cell in which the polypeptide
 CC is produced. The polypeptide is especially one that is substantially

CC insoluble or inactive when expressed recombinantly without the peptide
 CC extension. The present sequence represents Bacteriophage T7 ssrA peptide,
 CC used in a fusion to demonstrate the method of the invention.

SQ Sequence 6 AA;
 Query Match 54.5%; Score 6; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Rattus sp.

QY 1 AANDEN 6
 |||||
 Db 1 AANDEN 6

RESULT 7
 AAW08376 standard; peptide; 11 AA.
 XX
 ID AAW08376
 AC AAW08376
 XX
 DT 30-MAR-1997 (first entry)
 DE Rat brain adenosine kinase peptide 5.
 XX Adenosine kinase; agonist; antagonist; monoclonal antibody.
 XX Rattus sp.
 OS
 PN WO9640937-A2.
 XX
 PD 19-DEC-1996.
 XX PP 31-MAY-1996; 96WO-US008097.
 XX PR 07-JUN-1995; 95US-00460019.
 XX (ABBO) ABBOTT LAB.
 XX
 PI Cowart MD, Halbert DN, Kerwin JF, McNally T;
 DR; 1997-052334/05.
 XX
 PT brain, and human placenta short and long forms of adenosine kinase -
 PT used, e.g., for assaying for AK (ant) agonists or for prodn. of monoclonal
 PT antibodies against AK.
 XX Disclosure: Fig 6a; 75pp; English.

XX Adenosine kinase (AK) (AAW08369) purified from rat brain was digested
 CC with endoprotease Arg C, and peptide fragments were separated by HPLC. 5
 CC Peptides were sequenced (AAW08372-76). Internal portions of peptides 2
 CC and 4 were used to design degenerate primers (see also AAT48846-47) that
 CC were utilised in the identification of rat brain DNA clones (see also
 CC AAT48843) coding for AK (AAW08369).

SQ Sequence 11 AA;
 Query Match 45.5%; Score 5; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
 |||||
 Db 4 YAASV 8

RESULT 8
 AAW73649 standard; protein; 11 AA.
 XX
 AC AAW73649
 XX

DT 23-MAR-1999 (first entry)
 XX Rat adenosine kinase protein fragment.
 DE
 XX
 KW Adenosine kinase; cytotoxic nucleoside resistance; anticancer; antiviral;
 KW liver tumour; gout; acquired immune deficiency syndrome; tissue injury;
 KW adenosine concentration; cytoprotection; rat.
 XX
 OS
 XX
 PN US5561294-A.
 XX
 PD 19-JAN-1999.
 XX
 PF 07-JUN-1995; 95US-00479614.
 XX
 PR 07-JUN-1995; 95US-00479614.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Halbert DN, Kerwin JF, McNally T, Cowart MD;
 XX
 DR; 1999-130392/11.
 XX
 PT New nucleic acid encoding adenosine kinases and related oligo-nucleotides
 PT - expression vectors and transformed cells, used to modulate adenosine
 PT levels and to screen for specific modulators.
 XX
 Disclosure: Fig 6; 39pp; English.
 PS
 XX
 CC This sequence is a fragment of the rat brain adenosine kinase (AK) of the
 CC invention. Cells transformed with the DNA are used to produce recombinants;
 CC AK. The AK is used: (i) to screen for specific agonists and antagonists;
 CC (ii) to raise antibodies; and (iii) therapeutically (reduced levels of AK
 CC are associated with resistance to nucleoside analogues with cytotoxic,
 CC anticancer and antiviral properties, with liver tumours, gout and
 CC acquired immune deficiency syndrome). Fragments of the DNA sequence are
 CC used as primers and probes to screen DNA libraries and for identifying AK
 CC -encoding nucleic acid, also as antisense therapeutics (particularly to
 CC increase local adenosine concentrations at the site of tissue injury,
 CC increasing the level of cytoprotection)
 XX
 SQ Sequence 11 AA;
 Query Match 45.5%; Score 5; DB 2;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YAASV 11
 |||||
 Db 4 YAASV 8

RESULT 9
 AAU02541

ID AAU02541 standard; peptide; 16 AA.
 XX
 AC AAU02541;
 XX
 DT 29-AUG-2003 (revised)
 DT 23-APR-2002 (first entry)

XX Llama CDR2 region variable heavy chain fragment #34.
 KW
 KW Llama; phage display library; variable heavy domain fragment; VH; VH;
 KW sdAb fragment; single domain anti-idiotypic antibody fragment; CDR1/H1; CDR2;
 KW phage display technology; immune system response; CDR1/H1; CDR3;
 KW complementarity determining region.
 XX
 OS
 XX
 PN WO20010190-A2.
 XX
 Lama glama.
 XX
 AC
 XX

PS Claim 16; Page 32; 46pp; English.
 XX The present invention relates to a phage display library of variable
 CC heavy domain (VHH or VH) fragments (sdab fragments) derived from llama
 CC antibodies. The library is useful for in vitro selection against any
 CC antigen of interest as a target. Single domain anti-idiotypic antibody
 CC fragments are isolated from the library using phage display technology
 CC and an antibody serving as an antigen. Such anti-idiotypic antibody
 CC fragments have great potential in evoking the immune system response to
 CC pathological antigens and in vaccine development. The large size of the
 CC library considerably increases the probability of isolating from it
 CC antigen-binding fragments having high affinity to almost any
 CC predetermined target (antigen of interest). The library eliminates the
 CC development of anti-idiotypic antibodies by immunisation and allows
 CC isolation of anti-idiotypic antibodies AAU82435-AAU82635 represent the
 CC llama heavy chain domain fragments of the invention. (Updated on 29-AUG-
 XX 2003 to standardise OS field)
 SQ Sequence 17 AA;
 Query Match 45.5%; Score 5; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Query 7 YAASV 11
 DB 11 YAASV 15

RESULT 13
 ABP#2282
 ID ABP#2282 standard; peptide; 18 AA.
 XX
 AC ABP#2282;
 XX DT 10-OCT-2002 (first entry)
 XX DE Human immunopeptide to HCV E2 glycoprotein heavy chain CDR #52.
 XX KW Virucide; human; immunopolyptide; immunopeptide; envelope glycoprotein;
 XX KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
 XX KW NS3 protein; viral infection.
 XX Homo sapiens.
 XX PN WO200259340-A1.
 XX PD 01-AUG-2002.
 XX PF 25-JAN-2002; 2002WO-US002303.
 XX PR 26-JAN-2001; 2001US-0264451P.
 XX PA (SCRIB) SCRIPPS RES INST.
 XX PI Maruyama T, Jones IM, Burton DR, Fox RI;
 XX DR WPI; 2002-599001/64.
 XX PT New human immunopolyptide with binding specificity for certain envelope
 XX PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
 XX PT diagnosing or treating patients having or suspected of having HCV
 XX infection.
 XX PS Claim 17; 308pp; English.
 XX The present invention relates to human immunopolyptides, produced by a
 CC phase transfected cell library. The present sequence is one such
 CC immunopolyptide. The immunopolyptides have binding specificity for
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target
 CC cell binding and contains neutralising epitopes, while NS3 is thought to
 CC be involved in the replication of HCV. The immunopolyptides are useful
 CC for diagnosing and treating a patient having or suspected to be having
 CC HCV infection
 XX Sequence 18 AA;
 Query Match 45.5%; Score 5; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PS Disclosure; Page 19a; 46pp; English.
 XX The present invention relates to a phage display library of variable
 CC heavy domain (VHH or VH) fragments (sdab fragments) derived from llama
 CC antibodies. The library is useful for in vitro selection against any
 CC antigen of interest as a target. Single domain anti-idiotypic antibody
 CC fragments are isolated from the library using phage display technology
 CC and an antibody serving as an antigen. Such anti-idiotypic antibody

Qy 7 YAA SV 11
 Db 12 YAA SV 16

RESULT 14
 AAW16584
 ID AAW16584 standard; peptide; 19 AA.
 AC AAW16584;
 XX
 DT 30-NOV-1997 (first entry)
 DE Anti-RSV F glycoprotein antibody RSVF2-5 VH3 CDR2.
 XX
 KW Respiratory syncytial virus; RSV; monoclonal antibody; CDR;
 KW complementarity determining region; pneumonia; bronchiolitis; diagnosis;
 KW therapy; vaccine; RSVF2-5.
 OS Homo sapiens.
 XX
 PN WO9710846-A1.
 XX
 PD 27-MAR-1997.
 XX
 PP 18-SEP-1996; 96WO-US014931P.
 PR 18-SEP-1995; 95US-0003931P.
 XX
 PA (INTR-) INTRACEL CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Pilkington GR, Gilmour PS, Chanock RM, Crowe JE, Murphy BR;
 XX
 DR; 1997-202621/18.

PT Composition comprising respiratory syncytial virus antibody - useful for treatment or prophylaxis of active disease or infection.

PR
 PT
 PS 48-49; 71pp; English.

This peptide sequence comprises complementarity determining region 2 (CDR2) of the heavy chain VH3 sequence of a novel neutralising human monoclonal antibody to respiratory syncytial virus (RSV). The antibody, designated RSVF2-5 (ATCC 6909), selectively binds to an RSV F glycoprotein epitope, DNA encoding RSVF2-5 Fd and light chain (see AAT66586-57) was isolated from a phage library prepared from the RNA of peripheral blood lymphocytes of an HIV-1 infected donor. A claimed pharmaceutical preparation comprises a carrier and an antibody that includes the RSVF2-5 VH3 CDR3 (AAW16586) and which may also include the VH3 CDR2 and/or CDR1 (AAW16582) or the entire Fd region (AAW16580), or is an Fab fragment and further includes the RSVF2-5 VL6 CDR3 (AAW16594), CDR2 (AAW16592), CDR1 (AAW16590) or entire light chain (AAW16588). The preparation alternatively comprises a carrier and a vector that includes a nucleotide sequence encoding the antibody. The preparations can be used for the treatment or prophylaxis of active RSV disease or infection.

CC (claimed), and may also be used for RSV detection. The antibody binds and neutralises antigenic subgroups A and B of RSV with high efficiency

XX
 SQ Sequence 19 AA;

Query Match 45.5%; Score 5; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAA SV 11
 Db 13 YAA SV 17

Search completed: May 5, 2005, 18:18:07
 Job time : 103.333 secs

RESULT 15
 AAY05048

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Run on:	May 5, 2005, 18:10:34 ; Search time 20.3333 Seconds (without alignment(s))	52.052 Million cell updates/sec	callifMRPamide 8 - penalbumin - Adelin blood cell protein Ig heavy chain CRD venom protein HR-3		
Title:	US-10-827-133-10	1	L-hydrophorin - Ja dihydrofolate - redu pepsin (EC 3.4.23. carnitine medium/l		
Perfect score:	11	AAENDENYAAVSV 11	tubulin 2 beta-3 C 5-aminoimidazole r 19 Gamma-2b chain		
Sequence:			hemocyanin 1 - gre preabsorbing anti photosystem II oxy		
Scoring table:	OLIGO Gapop 60.0 , Gapext 60.0		photosystem II oxy		
Searched:	283416 seqs, 96216763 residues				
Word size :	0				
Total number of hits satisfying chosen parameters: 11837					
Minimum DB seq length:	0				
Maximum DB seq length:	50				
Post-processing: Listing First 45 summaries					
Database :	PIR 79;*				
	1: pir1;*				
	2: pir2;*				
	3: pir3;*				
	4: pir4;*				
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
-	-	-	-	-	-
1	4	36.4	19	B61056	cytochrome P450 PB probable 7-ethoxycoumarin O-deethylase (EC 1.14.14.-) cytochrome P450 isoform 1 - chick somatin - sorghum
2	4	36.4	20	S10680	hypothetical prote hypothetical prote ribosomal protein CAT-66 - Bacillus
3	4	36.4	22	B33174	N-carbamoyl-D-amino acid amidohydrolase probable 7-ethoxycoumarin O-deethylase (EC 1.14.14.-) cytochrome P450 isoform 1 - chick somatin - sorghum
4	4	36.4	28	E81239	C;Species: Gallus gallus (chicken)
5	4	36.4	29	S10050	C;Species: Gallus gallus (chicken)
6	4	36.4	30	I39799	C;Species: Gallus gallus (chicken)
7	4	36.4	30	S30333	C;Species: Gallus gallus (chicken)
8	4	36.4	32	F23454	R; Sinclair, J.F.; Wood, S.; Lambrecht, L.; Gorman, N.; Mende-Mueller, L.; Smith, L.; Hu Biochem. J. 269, 85-91, 1990
9	4	36.4	32	F60529	A;Title: Isolation of four forms of acetone-induced cytochrome P-450 in chicken liver b, A;Reference number: S10680; PMID:90328938; PMID:2375760
10	4	36.4	33	E81553	A;Accession: S10680 A;Molecule type: protein A;Residues: 1-20 <SIN>
11	4	36.4	34	A31564	C;Superfamily: cytochrome P450 homology C;Keywords: heme; membrane protein; microsome; monooxygenase; oxidoreductase
12	4	36.4	35	S22307	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13	4	36.4	37	RSPM81	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
14	4	36.4	37	PC1121	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
15	4	36.4	37	AH2787	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
16	4	36.4	38	S22210	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
17	4	36.4	38	A32790	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18	4	36.4	38	T14226	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19	4	36.4	38	I48924	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20	4	36.4	39	A80930	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
21	4	36.4	39	AF0836	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
22	4	36.4	40	A57482	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23	4	36.4	46	B45174	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
24	4	36.4	48	A84368	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
25	4	36.4	49	G44530	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
26	4	36.4	50	AC2028	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27	3	27.3	5	PT0281	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
28	3	27.3	5	A32014	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
29	3	27.3	6	PT0560	Query Match 36.4%; Score 4; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

sorghum - sorghum (fragment)
 C;Species: Sorghum bicolor (sorghum)
 C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 09-Jul-2004
 C;Accession: B33174
 R;Nijgers, A.J.; Roberts, W.K.; Selitrennikoff, C.P.
 Submitted to the Protein Sequence Database, May 1991
 A;Reference number: A33174
 A;Accession: B33174
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-22 <VIG>
 A;Cross-references: UNIPROT:Q9S908
 C;Superfamily: thaumatin I

Query Match 36.4%; Score 4; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
 Db 11 AASV 13

RESULT 6
 I39799
 CAT-66 - *Bacillus pumilus* (fragment)
 C;Species: *Bacillus pumilus*
 C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I39799
 R;Daval, E.J.; Williams, D.M.; Mongholksu, S.; Lovett, P.S.
 J. Bacteriol. 158, 784-790, 1984
 A;Title: Regulatory regions that control expression of two chloramphenicol-inducible cat
 A;Reference number: I39799; MUID:8421298; PMID:6327638
 A;Accession: I39799
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-30 <RES>
 A;Cross-references: UNIPROT:Q45356; GB:K01811; NID:gi142647; PIDN:AAA22292.1; PID:g551696

Query Match 36.4%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AASV 18

RESULT 7
 E81239
 hypothetical protein NMB0093 [imported] - *Neisseria meningitidis* (strain MC58) serogroup C;Species: *Neisseria meningitidis*
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: E81239
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Yamashita, J.; Gill, J.; Scariato, V.; Masignani, V.; Fizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: E81239
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-78 <TET>
 A;Cross-references: UNIPROT:Q9KL6; GB:AE002368; GB:AE002098; NID:97225303; PIDN:AAF4055
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0093

Query Match 36.4%; Score 4; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NDEN 6
 Db 3 NDEN 6

RESULT 5
 S10050
 ribosomal protein L19 - fission yeast (*Schizosaccharomyces pombe*) (fragment)
 N;Alternate names: ribosomal protein Sp-L15
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C;Accession: S10050
 R;Oraka, E.; Higo, K.I.; Itoh, T.
 Mol. Gen. Genet. 191, 519-524, 1983
 A;Title: Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from *Schizosaccha*
 A;Reference number: S07293; MUID:6355573
 A;Accession: S10050
 A;Molecule type: protein
 A;Residues: 1-29 <OTA>
 A;Cross-references: UNIPROT:P05734
 A;Superfamily: rat ribosomal protein L19
 C;Keywords: protein biosynthesis; ribosome

Query Match 36.4%; Score 4; DB 2; Length 29;

RESULT 8
 F23454
 ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)
 C;Species: *Dendrocygna bicolor* (fulvous whistling-duck)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C;Accession: F23454
 R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.
 Eur. J. Biochem. 114, 439-450, 1981
 A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.
 A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454
A;Molecule type: Protein
A;Residues: 1-32 <HEN>
A;Cross-references: UNIPROT:Q71ZD7
C;Superfamily: Serpin

Query Match 36.4%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 24 AASV 27

RESULT 9

F60529 hemocyanin M1 - crayfish (*Cherax destructor*) (fragment)
C;Species: *Cherax destructor* (yabby)
C;Accession: F60529
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
R;Neuteboom, B.; Sierdsema, S.J.; Beintema, J.J.
Comp. Biochem. Physiol. B 94: 587-592, 1989
A;Title: The relationship between N-terminal sequences and immunological characteristics
A;Reference number: A60529; MUID:90151075; PMID:2620501
A;Accession: F60529
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-32 <NEU>

Query Match 36.4%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NDEN 6
Db 27 NDEN 30

RESULT 10

E82553 hypothetical protein XP2468 [imported] - *Xylella fastidiosa* (strain 945c)
C;Species: *Xylella fastidiosa*
C;Accession: E82553
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R;anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406: 151-157, 2000
A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A;Reference number: A82515; MUID:20365717; PMID:10510347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession:E82553
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-33 <SIM>
A;Cross-references: UNIPROT:Q9PAM8; GB:AE004055; GB:AE003849; PIDN:AAF8526
A;Experimental source: strain 945c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvaranga, R.; Briones, E.R.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Froeh chdo, M.A.; Madeira, A.M.B.N.; Madeira, H.M.B.; Marino, C.L.; Marques, M.V.; Martins, E A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.P.M.; Miracca, B.C.; Miyaki, C.Y.; Rodrigues, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodriguez, V.; Rosa, A.J.de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; da Silva Jr., W.A.; da Silveir M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2468

Query Match 36.4%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 7 AASV 10

RESULT 11

A43564 neurogenic protein delta - fruit fly (*Drosophila melanogaster*) (fragment)
C;Species: *Drosophila melanogaster*
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43564
R;Haenlin, M.; Kramotskikh, B.; Campos-Ortega, J.A.
Development 110, 905-914, 1990
A;Title: The pattern of transcription of the neurogenic gene Delta of *Drosophila melanogaster*
A;Reference number: A43564; MUID:91209246; PMID:2128477
A;Accession: A43564
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-34 <HAE>
A;Cross-references: UNIPROT:Q95RM9
C;Genetics:
A;Gene: FlyBase:Dl
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology

Query Match 36.4%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 10 AASV 13

RESULT 12

S27307 surface-array protein - *Aeromonas hydrophila* (fragment)
C;Species: *Aeromonas hydrophila*
C;Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C;Accession: S27307; A33184
R;Kokka, R.P.; Vedros, N.A.; Janda, J.M.
J. Gen. Microbiol. 138, 1229-1236, 1992
A;Title: Immunochemical analysis and possible biological role of an *Aeromonas hydrophil* A;Reference number: S27307; MUID:92407495; PMID:1382113
A;Accession: S27307
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-35 <K02>
A;Cross-references: UNIPROT:Q9R5H9

Query Match 36.4%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 6 AASV 9

RESULT 13

R5PM81 ribosomal protein L36 - garden pea chloroplast
C;Species: chloroplastic ribosomal protein L36 in pea chloroplast
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A27301; S04382
R;Purton, S.; Gray, J.C.
Nucleic Acids Res. 15, 9080, 1987
A;Title: Nucleotide Sequence of the Gene for ribosomal protein L36 in pea chloroplast D
A;Reference number: A27301; MUID:3684583

A;Accession: A27301
A;Molecule type: DNA
A;Residues: 1-37 <PUR>
A;Cross-references: UNIPROT:F07815; GB:Y00468; NID:gi2162; PIDN:CAA68531.1; PID:gi2163
C;Genetics:
A;Gene: rpl36
A;Genome: chloroplast
C;Superfamily: Escherichia coli ribosomal protein L36
C;Keywords: chloroplast; protein biosynthesis; ribosome
F;1-37/Product: ribosomal protein L36a #status predicted <MAT>

Query Match Score 4; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 4 AASV 7

RESULT 14
PC1121
antifungal 25k_protein - flax (fragment)
C;Species: Linum usitatissimum (flax)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PC1121
R;Burgmeyer, J.R.; Smith, C.E.; Huynh, Q.K.,
Biochem. Biophys. Res. Commun. 187, 480-481, 1992
A;Title: Isolation and characterization of a 25 kDa antifungal protein from flax seeds.
A;Reference number: PC1121; MUID:92392370; PMID:1520338
A;Accession: PC1121
A;Molecule type: protein
A;Residues: 1-37 <BOR>
A;Cross-references: UNIPROT:Q9SBX1
A;Experimental source: seed
C;Suprafamily: thaumatin I
C;Keywords: antifungal

Query Match Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AASV 11
Db 15 AASV 18

RESULT 15
AH2787
hypothetical protein Atu1718 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH2787
R;Nood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.; Ergre, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-37 <KUR>
A;Cross-references: UNIPROT:Q8UEW7; GB:AE008688; PIDN:AAL42718.1; PID:gi17740156; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu1718
A;Map position: circular chromosome

Query Match Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 7e+02;

GenCore version 5.1.6									
Copyright (c) 1993 - 2005 Compugen Ltd.									
protein - protein search, using SW model									
on: May 5, 2005, 18:01:24 ; Search time 92:3333 Seconds (without alignments)									
61.006 Million cell updates/sec									
Allele: US-10-827-133-10 Effect score: 11 AANDENYAAV 11 Reference:									
String table: OLIGO Gapop 60.0 , Gapext 60.0									
Searched: 1612378 seqs, 512079187 residues									
Size : 0									
Total number of hits satisfying chosen parameters:									
Minimum DB seq length: 0 Maximum DB seq length: 50									
Post-processing: Listing first 45 summaries									
Database : UniProt_03_*									
1: uniprot_sprot:*									
2: uniprot_trembl:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Query Score Match Length DB ID Description									
1	8	72.7	26	2	Q9UC79	Q9UC79 homo sapien	Q9UC79	PRELIMINARY;	PRT; 26 AA.
2	7	63.6	10	2	P96306	P96306 aeromonas s	P96306	PRELIMINARY;	PRT; 13, Created
3	7	63.6	10	2	P96321	P96321 escherichia	P96321	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
4	7	63.6	10	2	P96352	P96352 marinobacte	P96352	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
5	7	63.6	10	2	Q931E5	Q931E5 photobacter	Q931E5	DE Interleukin-2 high-molecular-weight form (Fragment).	DE Interleukin-2 high-molecular-weight form (Fragment).
6	5	45.5	14	2	P92350	P92350 legionella	P92350	OS Homo sapiens	OS Homo sapiens
7	5	45.5	40	2	Q925P9	Q925P9 rickettsia	Q925P9	GO:0005576; C:extracellular; IEA.	GO; GO:0005576; C:extracellular; IEA.
8	4	36.4	10	2	P96421	P96421 newcastle d	P96421	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
9	4	36.4	13	2	Q718T2	Q718T2 neisseria g	Q718T2	PFAM: PF00715; IL2; 1.	PFAM: PF00715; IL2; 1.
10	4	36.4	15	2	Q9DWH6	Q9DWH6 thermococcu	Q9DWH6	SEQUENCE 26 AA; 2887 MW; 5B768892229356ED CRC64;	SEQUENCE 26 AA; 2887 MW; 5B768892229356ED CRC64;
11	4	36.4	15	2	QBWNX5	QBWNX5 arabidopsis	QBWNX5	Query Match Best Local Similarity 72.7% Score 8; DB 2; Length 26; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	Query Match Best Local Similarity 100.0% Score 8; DB 2; Length 26; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
12	4	36.4	18	1	SODM MYCHA	SODM MYCHA	SODM MYCHA	Q9UC79	Q9UC79
13	4	36.4	19	2	Q99RN2	Q99RN2 mycobacteri	Q99RN2	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
14	4	36.4	19	2	Q71ZJ0	Q71ZJ0 rattus norvegicus	Q71ZJ0	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
15	4	36.4	20	1	OPMP_VIBAL	OPMP_VIBAL	OPMP_VIBAL	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
16	4	36.4	20	2	QBM132	QBM132 vibrio algi	QBM132 vibrio algi	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
17	4	36.4	20	2	Q9RJD9	Q9RJD9 escherichia coli	Q9RJD9 escherichia coli	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
18	4	36.4	22	2	Q9DWH5	Q9DWH5 pyrococcus	Q9DWH5 pyrococcus	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
19	4	36.4	22	2	Q9SSP13	Q9SSP13 sorghum bicolor	Q9SSP13 sorghum bicolor	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
20	4	36.4	22	2	Q85513	Q85513 chlamydia trachomatis	Q85513 chlamydia trachomatis	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
21	4	36.4	22	2	OB5515	OB5515 chlamydia trachomatis	OB5515 chlamydia trachomatis	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
22	4	36.4	22	2	Q9RAW9	Q9RAW9 burkholderi	Q9RAW9 burkholderi	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
23	4	36.4	23	2	Q53469	Q53469 mycobacteri	Q53469 mycobacteri	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
24	4	36.4	23	2	Q7RQ41	Q7RQ41 plasmidium	Q7RQ41 plasmidium	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
25	4	36.4	27	2	Q9GPK7	Q9GPK7 scutigerell	Q9GPK7 scutigerell	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
26	4	36.4	27	2	Q99N99	Q99N99 zea mays	Q99N99 zea mays	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
27	4	36.4	27	2	Q66269	Q66269 cucumber mo	Q66269 cucumber mo	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
28	4	36.4	27	2	Q9HC3	Q9HC3 hepatitis c	Q9HC3 hepatitis c	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
29	4	36.4	27	2	Q9QBC6	Q9QBC6 hepatitis c	Q9QBC6 hepatitis c	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
30	4	36.4	27	2	Q9QBC7	Q9QBC7 hepatitis c	Q9QBC7 hepatitis c	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.
31	4	36.4	27	2	Q9QBC8	Q9QBC8 hepatitis c	Q9QBC8 hepatitis c	DR InterPro; IPR00779; Interleukin-2.	DR InterPro; IPR00779; Interleukin-2.

RL RNA 2:1306-1310(1996).
DR EMBL; U65075; AAB49322..1; -.
FT NON TER 1 1 MW; . 857BD22DCB544B1A CRC64;
SQ SEQUENCE 10 AA; 1051 MW; . 857BD22DCB544B1A CRC64;

Query Match 63.6%; Score 7; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 3
P96321 PRELIMINARY; PRT; 10 AA.
ID P96321; PRELIMINARY;
AC P96321; 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAY-1997 (TREMBLrel. 03, Last annotation update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DB Coded portion of proteolysis tag (Fragment).
OS Photobacterium phosphoreum.
RA Williams K.P.; Barriel D.P.;
RT "Phylogenetic analysis of tRNA secondary structure.";
RN PNA 2:1306-1310(1996).
RN [1]
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 133;
RC MEDLINE=9128184; PubMed=8972778;
RA Williams K.P.; Barriel D.P.;
RT "Phylogenetic analysis of tRNA secondary structure.";
RN PNA 2:1306-1310(1996).
RN [1]
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=95023983; PubMed=7524073;
RA Komine Y.; Kitabatake M.; Yokogawa T.; Nishikawa K.; Inokuchi H.;
RT "A tRNA-like structure is present in 10S rRNA, a small stable RNA from
Escherichia coli.";
RT Escherichia coli.; Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227 (1994).
RL EMBL; U65074; AAB48024..1; -.
FT NON TER 1 1 MW; . 857BD22DCB544B1A CRC64;
SQ SEQUENCE 10 AA; 1051 MW; . 857BD22DCB544B1A CRC64;

Query Match 63.6%; Score 7; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 5
P931E5 PRELIMINARY; PRT; 10 AA.
ID P931E5; PRELIMINARY;
AC P931E5; 03, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Proteolysis tag (Fragment).
OS Photobacterium phosphoreum.
RA Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;
OC Vibionaceae; Photobacterium.
OC NCB!_TaxID=652;
OX NCBI_TaxID=652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=10061247; PubMed=10592213; DOI=10.1093/nar/28.1.168;
RA Williams K.P.;
RT "The tmRNA website."
RL Nucleic Acids Res. 28:168-168 (2000).
RN [2]
RN SEQUENCE FROM N.A.
RA Williams K.P.;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL DR EMBL; AY040837; AAK83555..1; -.
FT NON TER 1 1 MW; . 857BD22DCB544B1A CRC64;
SQ SEQUENCE 10 AA; 1051 MW; . 857BD22DCB544B1A CRC64;

Query Match 63.6%; Score 7; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 6
P96350 PRELIMINARY; PRT; 14 AA.
ID P96350; PRELIMINARY;
AC P96350; 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Legionella pneumophila.
RA Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33152;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P.; Barriel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).
DR EMBL; U68079; AAB48026..1; -.
FT NON TER 1 1 MW; . 1349 MW; CE557318D3BE7DD CRC64;
SQ SEQUENCE 14 AA; 1349 MW; CE557318D3BE7DD CRC64;

Query Match 45.5%; Score 5; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Qy 2 ANDENYA 8
Db 1 ANDENYA 7

RESULT 4
P96352 PRELIMINARY; PRT; 10 AA.
ID P96352; PRELIMINARY;
AC P96352; 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Marinobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97128184; PubMed=8972778;
RA Williams K.P.; Barriel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure.";
RL RNA 2:1306-1310(1996).

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	2 ANDEN 6 1 ANDEN 5									
Db										
RESULT 7: Q925P9 PRELIMINARY; PRT; 40 AA.										
AC	Q925P9	ID	01-DEC-2001 (TREMBLrel. 19, Created)	DT	01-JUN-2003 (TREMBLrel. 19, Last sequence update)	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DB	Adenosine kinase (BC 2.7.1.20) (Fragment).	
OS	Cricetulus griseus (Chinese hamster).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Crictetinae.	OC		NCBI_TaxID=10029;	RN			
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	RA	Medline=21134654; PubMed=11242543;	RA	Singh B., Lin A., Wu Z.C., Gupta R.S.; "Gene structure for adenosine kinase in Chinese hamster and human: high-frequency mutants of CHO cells involve deletions of several introns and exons.";	RA		
RN	[1]	RP	SEQUENCE FROM N.A.	RA	PubMed=8917457;	RA	"Cloning and characterization of cDNA for adenosine kinase from mammalian (Chinese hamster, mouse, human and rat) species. High frequency mutants of Chinese hamster ovary cells involve structural alterations in the gene.";	RA		
DR	EMBL; AF284092; AAK55961.1; -.	DR	EMBL; AF284092; AAK55961.1; -.	DR	GO; GO:000401; F:adenosine kinase activity; IEA.	DR	GO; GO:0016301; F:kinase activity; IEA.	DR	GO; GO:0016740; F:transferase activity; IEA.	DR
FT	NON_TER 1	FT	NON_TER 1	FT	Kinase; Transferase.	FT	NON_TER 1	FT	NON_TER 1	FT
SQ	SEQUENCE 40 AA; 4580 MW; C8B865B246E807036 CRC64;	SQ	SEQUENCE 40 AA; 4580 MW; C8B865B246E807036 CRC64;	SQ						
RESULT 8: P96421 PRELIMINARY; PRT; 10 AA.										
AC	P96421	ID	01-MAY-1997 (TREMBLrel. 03, Created)	AC	01-MAY-1997 (TREMBLrel. 03, Last sequence update)	DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)	DB	Coded portion of proteolytic tag (Fragment).	
Qy	7 YAAV 11 1	Qy	7 YAAV 11	Db	20 YAAV 24	Db		OS	Neisseria gonorrhoeae.	
Db		Db		OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.	OC		RA		
RN	[1]	RN		RA	NCBI_TaxID=485;	RN	SEQUENCE FROM N.A.	RA	STRAIN=ATCC 19424;	RA
RP		RP		RA	Medline=97128184; PubMed=8972778;	RP	SEQUENCE FROM N.A.	RA	Williams K.P., Bartel D.P.; "Phylogenetic analysis of tRNA secondary structure."	RT
RC		RC		RA		RC	Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4;	RA		
RT		RT		RT		RT	Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 4;	RT		
SQ	SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;	SQ	SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;	SQ		SQ	Score 4; DB 2; Length 15;	SQ		
RESULT 9: Q718T2 PRELIMINARY; PRT; 13 AA.										
ID	Q718T2	ID	01-DEC-2004 (TREMBLrel. 27, Created)	AC	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	DB	DE Hemagglutinin-neuraminidase (Fragment).	
Qy	2 ANDE 5 1 ANDE 4	Qy	2 ANDE 5	Db	1 ANDE 4	Db		OS	Newcastle disease virus.	
Db		Db		OC	Paramyxoviridae; Paramyxovirinae; Avulavirus.	OC		RA		
RN	[1]	RN		RA	NCBI_TaxID=11176;	RA	SEQUENCE FROM N.A.	RA		
RP		RP		RA	Gould A.R., Hansson, B., Selleck K., Kattenbelt J.A., Mackenzie M., Della-Porta A.J.; "Newcastle disease virus fusion and hemaggglutinin-neuraminidase gene motifs as markers for viral lineage.";	RA		RT		
RT		RT		RT	"Newcastle disease virus fusion and hemaggglutinin-neuraminidase gene motifs as markers for viral lineage.";	RT		RL		
RT		RT		RL	Avian Pathol. 32:361-373 (2003).	RL		DR		
RT		RT		DR	AF542841; AAQ11561.1; -.	DR		FT		
RT		RT		FT	NON_TER 1	FT		SQ	SBQQUENCE 13 AA; 1628 MW; 685A333609B645BB CRC64;	FT
RT		RT		SQ	SEQUENCE 13 AA; 1628 MW; 685A333609B645BB CRC64;	SQ				
RESULT 10: Q9UWH6 PRELIMINARY; PRT; 15 AA.										
ID	Q9UWH6	ID	01-MAY-2000 (TREMBLrel. 13, Created)	AC	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT	01-MAY-2000 (TREMBLrel. 14, Last annotation update)	DB	Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha (Fragment).	
Qy	7 YAAS 10 1	Qy	7 YAAS 10	Db	8 YAAS 11	Db		OS	Thermococcus litoralis.	
Db		Db		OC	Buryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.	OC		RA		
RN	[1]	RN		RA	NCBI_TaxID=2265;	RA		RT		
RP		RP		RA	Medline=96146528; PubMed=8550513;	RA		RT		
RX		RX		RA	Heider J., Mai X., Adams M.W.; "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a new and reversible coenzyme A-dependent enzyme involved in peptide fermentation by hyperthermophilic archaea."	RA		RT		
RT		RT		RT	Sequel. 178:780-787 (1996).	RT		RL		
RT		RT		RL	SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;	RL		SQ		
SQ		SQ		SQ	SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;	SQ				
RESULT 11: Q9UWH6 PRELIMINARY; PRT; 15 AA.										
ID	Q9UWH6	ID	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	AC	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	DB	Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha (Fragment).	
Qy	7 YAASV 11 1	Qy	7 YAASV 11	Db	20 YAASV 24	Db		OS	Thermococcus litoralis.	
Db		Db		OC	Buryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.	OC		RA		
RN	[1]	RN		RA	NCBI_TaxID=485;	RA		RT		
RP		RP		RA	Strain=ATCC 19424;	RA		RT		
RC		RC		RA	Medline=97128184; PubMed=8972778;	RA		RT		
RT		RT		RA	Williams K.P., Bartel D.P.; "Phylogenetic analysis of tRNA secondary structure."	RA		RT		
SQ		SQ		SQ	SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;	SQ				

	Qy	SQ	SEQUENCE	18 AA;	1883 MW;	A4161A3DAC93F710 CRC64;
	Db	6 NYAA 9 				
	Db	8 NYAA 11 				
RESULT 11						
	QBW4X5	PRELIMINARY;	PRT;	15 AA.		
	ID					
	QBW4X5;					
	AC					
	Q8M4X5;					
	DT 01-MAR-2002	(TREMBrel. 20, Created)				
	DT 01-MAR-2002	(TREMBrel. 20, Last sequence update)				
	DT 01-MAR-2002	(TREMBrel. 20, Last annotation update)				
	DE Ch13/nitrate reductase structural protein (Fragment).					
	GN Name=N142;					
	OS Arabidopsis thaliana (Mouse ear cress).					
	OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;					
	OC Spermatophytina; Magnoliophytina; eudicots; rosids;					
	NCBI_TaxID=3702;					
	RN [1]					
	RP SEQUENCE FROM N.A.; PubMed=1840922;					
	RX MEDLINE=93005711; PubMed=1840922;					
	RA Wilkison J.Q., Crawford N.M.;					
	RT "Identification of the Arabidopsis CHU3 gene as the nitrate reductase structural gene NIA2.";					
	RT Plant Cell 3:461-471 (1991).					
	DR EMBL; S45384; AAL32272.1; -.					
	DR NON_TER 15 FT 15 AA; 1721 MW;	71C901FC029E1CFD CRC64;				
	SEQUENCE 15 AA;					
	Qy	Query Match Score 4; Best Local Similarity 100.0%; Matches 4;	DB 2; Pred. No. 1.6e+03; Conservative 0;	Length 15; Indels 0; Gaps 0;		
	Db	8 AASV 11 2 AASV 5				
RESULT 12						
	SODM_MYCHA	STANDARD;	PRT;	18 AA.		
	ID					
	SODM_MYCHA					
	AC P80382;					
	DT 01-OCT-1996	(Rel. 34, Created)				
	DT 01-OCT-1996	(Rel. 34, Last sequence update)				
	DT 05-JUL-2004	(Rel. 44, Last annotation update)				
	DE Superoxide dismutase [Mn] (Bc 1.15.1.1) (Fragment).					
	GN Name=sodB; Synonyms=sod;					
	OS Mycobacterium habana.					
	OC Bacteria; Actinobacteria; Actinomycetales;					
	OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.					
	NCBI_TaxID=1784;					
	RN [1]					
	RP SEQUENCE,					
	RC STRAIN=EMC 5135;					
	RX MEDLINE=96262109; PubMed=8704977;					
	RA Bish D., Mehrotra J., Dhindola M.S., Singh N.B., Sinha S.;					
	RT "A major T-cell-inducing cytosolic 23 kDa protein antigen of the vaccine candidate Mycobacterium habana is superoxide dismutase";					
	RT Microbiology 142:1375-1383 (1996).					
	CC -!- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.					
	CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H ⁺ = O ₂ + H ₂ O ₂ .					
	CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).					
	CC -!- SUBUNIT: Homodimer (Probable).					
	CC -!- SUBCELLULAR LOCATION: Cytoplasmic.					
	CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.					
	DR InterPro: IPR001189; Sodisomerase.					
	DR Pfam; PF0081; Sod_Fe_N; 1.					
	PROSITE PS0088; SOD_MN; PARTIAL.					
	KW Direct protein sequencing; Manganese; Metal-binding; Oxidoreductase.					
	FT NON_TER 18					
	Qy	Query Match Score 4; Best Local Similarity 100.0%; Matches 4;	DB 2; Pred. No. 2e+03; Conservative 0;	Length 19; Indels 0; Gaps 0;		
	Db	8 AASV 11 6 AASV 9				

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RESULT 15
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ID  P83151          (Rel. 41; Created)
AC
DT  28-FEB-2003   (Rel. 41; Last sequence update)
DT  05-JUL-2004   (Rel. 44; Last annotation update)
DB  Outer membrane protein W (Outer membrane protein 25Va) (Omp25Va)
DB  (Fragment).
GN  Name=ompW;
GN  Name=ompW;
OS  Vibrio alginolyticus
OS  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC  Vibrionaceae; Vibrio.
NCBI_TAXID=663;
RN  [1]
RN  SEQUENCE.
RP  STRAIN=NCIMB 1903T;
RC  Onji M., Hirabayashi J., Suzuki S.;
RT  "Characterization of major outer membrane proteins of Vibrio
    alginolyticus and the stability against proteases." ;
RT  Microbes Environ. 0:0-0 (2002).
RL  -!- SUBCELLULAR LOCATION: Outer membrane.
CC  -!- SIMILARITY: Belongs to the ompW/alkL family.
KW  Direct protein sequencing; Outer membrane.
FT  NON_TER 20 20
SQ  SEQUENCE 20 AA;  2096 MW;  D29EE7FC0A16C0D37 CRC64;
Query Match 36.4%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy  8 AASV 11
Db  ||||| 12 AASV 15

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Search completed: May 5, 2005, 18:22:52
Job time : 94.333 sec

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2	8	72.7	11	3	US-09-045-585-1	Sequence 1, Appli	Best Local Similarity 100.0%; Pred. No. 0.025;
3	8	72.7	11	4	US-09-953-321-1	Sequence 1, Appli	Mismatches 0; Indels 0; Gaps 0;
4	8	72.7	11	4	US-08-756-416-1	Sequence 1, Appli	
5	5	45.5	29	4	US-09-270-767-36486	Sequence 36486, A	Qy 1 AANDENYA 8
6	5	45.5	29	4	US-09-270-767-51703	Sequence 51703, A	Db 1 AANDENYA 8
7	5	45.5	30	2	US-08-244-657-1	Sequence 1, Appli	
8	5	45.5	31	3	US-09-227-357-398	Sequence 398, App	
9	9	45.5	41	4	US-09-493-798B-316	Sequence 316, App	
10	4	36.4	4	1	US-08-777-208-1	Sequence 1, Appli	RESULT 2
11	4	36.4	5	3	US-09-125-51A-46	Sequence 46, Appli	US-09-425-585-1
12	4	36.4	5	3	US-09-284-625-10	Sequence 1, Appli	; Sequence 1, Application US/09425585
13	4	36.4	5	4	US-08-877-605-324	Sequence 324, App	; General Information:
14	4	36.4	5	6	5217869-7-3	Patent No. 5217869	; Applicant: PLUCKHUN, ANDREAS
15	4	36.4	5	6	5217869-7-3	Patent No. 5217869	; Title of Invention: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
16	4	36.4	6	3	US-09-125-517A-5	Sequence 5, Appli	; File Reference: PLUCK/1
17	4	36.4	6	3	US-08-185-355B-25	Sequence 25, Appli	; Current Application Number: US/09/425, 585
18	4	36.4	6	4	US-08-877-605-315	Sequence 315, App	; Current Filing Date: 1998-10-22
19	4	36.4	6	4	US-08-877-605-334	Sequence 334, App	; Prior Application Number: PCT/EP98/02420
20	4	36.4	7	4	US-08-877-605-342	Sequence 342, App	; Prior Filing Date: 1998-04-23
21	4	36.4	8	3	US-08-688-988-48	Sequence 48, App	; Number of SEQ ID NOS: 15
22	4	36.4	8	6	5436138-14	Patent No. 5436138	; Software: PatentIn Ver. 2.1
23	4	36.4	8	6	5436138-14	Sequence 2, Appli	; SEQ ID NO: 1
24	4	36.4	9	1	US-08-180-547A-2	Sequence 2, Appli	; LENGTH: 11
25	4	36.4	9	2	US-08-250-847B-2	Sequence 2, Appli	; TYPE: PRT
26	4	36.4	9	2	US-08-408-095-4	Sequence 4, Appli	
27	4	36.4	9	2	US-08-463-949A-2	Sequence 2, Appli	

ALIGNMENTS

Total number of hits satisfying chosen parameters: 272444

RESULT 1
US-09-056-105-33

; Sequence 33, Application US/09056105

; Patent No. 6287569

; GENERAL INFORMATION:

; APPLICANT: KIPPS, THOMAS J.

; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

; TITLE OF INVENTION: PROCESSING

; FILE REFERENCE: 233/221

; CURRENT APPLICATION NUMBER: US/09/056,105

; CURRENT FILING DATE: 1998-04-06

; EARLIER APPLICATION NUMBER: 60/043,467

; EARLIER FILING DATE: 1997-04-10

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO: 33

; LENGTH: 11

; TYPE: PRT

; ORGANISM: E.Coli

; US-09-056-105-33

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; ORGANISM: Escherichia coli
; US-09-425-585-1

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Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AANDENYA 8
Db      1 AANDENYA 8

RESULT 3
US-09-953-321-1.
; Sequence 1, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOSEPH
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCKA1 CON2
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/953,321
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-953-321-1.

Query Match          72.7%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AANDENYA 8
Db      1 AANDENYA 8

RESULT 4
US-09-756-416-1.
; Sequence 1, Application US/08756416
; Patent No. 6699715
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha
; APPLICANT: Feil, Perry
; APPLICANT: Mittler, Robert
; APPLICANT: Winberg, Gosta
; TITLE OF INVENTION: MODIFIED SFV MOLECULES WHICH
; TITLE OF INVENTION: MEDIATE ADHESION BETWEEN CELLS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merchant & Gould
; STREET: 11150 Santa Monica, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,416
; FILING DATE: 27-NOV-1996
; CURRENT APPLICATION NUMBER: US/09-756-416-1
; FILING DATE: 09-09-1999
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51703
; LENGTH: 29

RESULT 5
US-09-270-767-36486
; Sequence 36486, Application US/09270767
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; Patent No. 6703491
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SEQ ID NO 36486
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; US-09-270-767-36486

RESULT 6
US-09-270-767-51703
; Sequence 51703, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51703
; LENGTH: 29

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i ORGANISM: Drosophila melanogaster
i US-09-270-767-51703

Query Match 45.5%; Score 5; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10
Db 10 NYAAA 14

RESULT 7
US-08-244-657-1

/ Sequence 1, Application US/08244657

/ Patent No. 5902736

/ GENERAL INFORMATION:

/ APPLICANT: YAMADA, Hideaki

/ APPLICANT: SHIMIZU, Sakayu

/ APPLICANT: IKENAKA, Yasuhiro

/ APPLICANT: YAJIMA, Kazuyoshi

/ APPLICANT: YAMADA, Yukio

/ APPLICANT: NANEI, Hirokazu

/ APPLICANT: TAKANO, Masayuki

/ APPLICANT: TAKAHASHI, Satomi

/ TITLE OF INVENTION: Process For The Production of D-a-Amino

/ TITLE OF INVENTION: Acids

/ NUMBER OF SEQUENCES: 3

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Foley & Lardner

/ STREET: 3000 K Street, N.W., Suite 500

/ CITY: Washington, D.C.

/ COUNTRY: USA

/ ZIP: 20007-5109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/244,657

/ FILING DATE: 06-JUN-1994

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: PCT/JP93/01408

/ FILING DATE: 01-OCT-1993

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: JP 265914/1992

/ FILING DATE: 05-OCT-1992

/ ATTORNEY/AGENT INFORMATION:

/ NAME: WEGNER, Harold C.

/ REGISTRATION NUMBER: 25,258

/ REFERENCE/DOCKET NUMBER: 74129/185/AOPA

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (202) 672-5300

/ TELEFAX: (202) 672-5399

/ TELEX: 904136

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 30 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ US-08-244-657-1

/ INFORMATION FOR SEQ ID NO: 2:

/ LENGTH: 30

/ TYPE: amino acid

/ TOPOLOGY: linear

/ US-08-244-657-1

/ INFORMATION FOR SEQ ID NO: 3:

/ LENGTH: 30

/ TYPE: amino acid

/ TOPOLOGY: linear

RESULT 8
US-09-27-357-398
/ Sequence 398, Application US/09227357

/ Patent No. 6342581

/ GENERAL INFORMATION:

/ APPLICANT: Fischer et al.

/ TITLE OF INVENTION: 123 Human Secreted Proteins

/ FILE REFERENCE: P2010PI

/ CURRENT APPLICATION NUMBER: US/09/227,357

/ CURRENT FILING DATE: 1999-01-08

/ EARLIER APPLICATION NUMBER: PCT/US98/13684

/ EARLIER FILING DATE: 1998-07-07

/ EARLIER APPLICATION NUMBER: 60/051,926

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,793

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,925

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,929

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,803

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,732

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,931

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,803

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,932

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,916

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,930

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,918

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,720

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,920

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,733

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,795

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,919

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,928

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,722

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,920

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,916

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,733

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,933

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/056,360

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,947

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,964

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,954

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/058,785

/ EARLIER FILING DATE: 1997-09-12

/ EARLIER APPLICATION NUMBER: 60/058,664

/ EARLIER FILING DATE: 1997-09-12

/ EARLIER APPLICATION NUMBER: 60/058,660

RESULT 8
US-09-27-357-398

/ Sequence 398, Application US/09227357

/ Patent No. 6342581

/ GENERAL INFORMATION:

/ APPLICANT: Fischer et al.

/ TITLE OF INVENTION: 123 Human Secreted Proteins

/ FILE REFERENCE: P2010PI

/ CURRENT APPLICATION NUMBER: US/09/227,357

/ CURRENT FILING DATE: 1999-01-08

/ EARLIER APPLICATION NUMBER: PCT/US98/13684

/ EARLIER FILING DATE: 1998-07-07

/ EARLIER APPLICATION NUMBER: 60/051,926

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,793

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,925

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,929

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,803

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,931

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,803

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,932

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,916

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,732

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,920

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,733

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,919

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,928

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/052,795

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/051,948

/ EARLIER FILING DATE: 1997-07-08

/ EARLIER APPLICATION NUMBER: 60/055,949

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,953

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,948

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,947

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,964

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/056,360

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,684

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,984

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/055,954

/ EARLIER FILING DATE: 1997-08-18

/ EARLIER APPLICATION NUMBER: 60/058,785

/ EARLIER FILING DATE: 1997-09-12

/ EARLIER APPLICATION NUMBER: 60/058,664

/ EARLIER FILING DATE: 1997-09-12

/ EARLIER APPLICATION NUMBER: 60/058,660

EARLIER FILING DATE: 1997-09-12
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/777,208
 FILING DATE: 27-DEC-1996
 CLASSIFICATION: 514
 PRIORITY INFORMATION:
 PRIORITY NUMBER: 08/539944
 FILING DATE: 06-OCT-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Colton, Laurence P.
 REGISTRATION NUMBER: 33371
 REFERENCE/DOCKET NUMBER: 10733-191B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 875-3555
 TELEFAX: (404) 875-8505
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: no
 US-08-777-208-1

RESULT 9
 US-09-493-795B-316
 Sequence 316 Application US/09493795B
 PRIORITY NUMBER: US 697808
 GENERAL INFORMATION:
 APPLICANT: Watkins, Maren
 APPLICANT: Olivera, Baldemero M.
 APPLICANT: Hillyard, David R.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Jones, Robert M.
 TITLE OF INVENTION: Alpha-Conotoxin Peptides
 FILE REFERENCE: 2314-179 A
 CURRENT APPLICATION NUMBER: US/09/493,795B
 CURRENT FILING DATE: 2000-01-28
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 404
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 316
 LENGTH: 41
 TYPE: PRF
 ORGANISM: Conus catulus
 US-09-493-795B-316

Query Match 45.5%; Score 5; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 6 NYAAA 10
 Db 14 NYAAA 18

RESULT 11
 US-09-125-517A-46
 Sequence 46 Application US/09125517A
 PRIORITY NUMBER: US 6087336
 GENERAL INFORMATION:
 APPLICANT: Cotton, Ronald
 APPLICANT: Edwards, Phillip Neil
 APPLICANT: Luke, Richard William Arthur
 TITLE OF INVENTION: Peptide Derivatives
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
 STREET: 555 Thirteenth St., N.W., Suite 701 East
 STREET: Tower
 CITY: Washington
 STATE: DC
 COUNTRY: U.S.A.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/125,517A
 FILING DATE: 20-AUG-1998
 CLASSIFICATION: 530
 PRIORITY INFORMATION:
 PRIORITY NUMBER: GB 9620819.4
 FILING DATE: 05-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Ernst, Barbara G.
 REGISTRATION NUMBER: 30,377
 REFERENCE/DOCKET NUMBER: 1991-127
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-783-6040
 TELEFAX: 202-783-6031
 INFORMATION FOR SEQ ID NO: 46:

RESULT 10
 US-08-777-208-1
 Sequence 1 Application US/08777208
 PRIORITY NUMBER: 5763576
 GENERAL INFORMATION:
 APPLICANT: Powers, James C.
 TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Deveau, Colton & Marquis
 STREET: Two Midtown Plaza, Suite 1400
 CITY: Atlanta
 STATE: GA
 COUNTRY: USA
 ZIP: 30309
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Microsoft Windows 95
 SOFTWARE: Microsoft Word

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SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-125-517A-46

Query Match          36.4%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      8 AAVV 11
Db      1 AAVV 4

RESULT 14
5217869-73
; PATENT NO. 5217869
; APPLICANT: KAVYAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255, 906
; FILING DATE: 11-OCT-1988
; SEQ ID NO: 73:
; LENGTH: 5

Query Match          36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 AAND 4
Db      2 AAND 5

RESULT 15
5217869-73
; PATENT NO. 5217869
; APPLICANT: KAVYAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255, 906
; FILING DATE: 11-OCT-1988
; SEQ ID NO: 73:
; LENGTH: 5

Query Match          36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 AAND 4
Db      2 AAND 5

RESULT 16
5217869-73
; PATENT NO. 5217869
; APPLICANT: KAVYAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255, 906
; FILING DATE: 11-OCT-1988
; SEQ ID NO: 73:
; LENGTH: 5

Query Match          36.4%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 AAND 4
Db      2 AAND 5

Search completed: May 5, 2005, 18:24:17
Job time : 29 secs

RESULT 17
Sequence 324, Application US/08877605
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 324
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Peptide Z Library
; OTHER INFORMATION: Peptide Z Library
; Query Match          36.4%; Score 4; DB 4; Length 5;
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Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2005, 18:18:20 ; Search time 78 Seconds
(without alignments)
47.046 Million cell updates/sec

Title: US-10-827-133-8
Perfect score: 11
Sequence: 1 AANDENYAAAV 11

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 1428551 seqs, 33359853 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4250592

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	72.7	11	9 US-09-953-321-1	Sequence 1, Appli
2	8	72.7	11	9 US-09-975-132A-3	Sequence 3, Appli
3	8	72.7	11	14 US-10-289-135A-119	Sequence 119, Appli
4	8	72.7	12	14 US-10-080-066-19	Sequence 19, Appli
5	6	54.5	6	14 US-10-037-243-3	Sequence 3, Appli
6	5	45.5	31	10 US-09-083-802-398	Sequence 398, Appli
7	5	45.5	31	10 US-09-190-398	Sequence 398, Appli
8	5	45.5	31	11 US-09-973-278-508	Sequence 508, Appli
9	5	45.5	41	17 US-10-895-372-316	Sequence 316, Appli
10	4	36.4	4	9 US-09-337-537B-1	Sequence 1, Appli
11	4	36.4	4	15 US-10-427-208-17	Sequence 17, Appli
12	4	36.4	6	10 US-09-991-662-25	Sequence 25, Appli
13	4	36.4	8	13 US-10-007-761-30	Sequence 30, Appli

RESULT 1
US-09-953-321-1
; Application US/09953321
; Patent No. US20020115083A1
; GENERAL INFORMATION:
; APPLICANT: PLUCHTHUN, ANDREAS
; APPLICANT: HANES, JOSEF
; APPLICANT: JEROMUTIS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; FILE REFERENCE: BLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-953-321-1

Query Match 72.7%; Score 8; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 AANDENYA 8
Db 1 AANDENYA 8

RESULT 2
US-09-975-132A-3
; Sequence 3, Application US/09975132A
; Publication No. US20020182672A1

ALIGNMENTS

Sequence 27, Appli
Sequence 27, Appli
Sequence 6, Appli
Sequence 31, Appli
Sequence 81, Appli
Sequence 94, Appli
Sequence 102, Appli
Sequence 1, Appli
Sequence 17, Appli
Sequence 29, Appli
Sequence 119, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 246, Appli
Sequence 246, Appli
Sequence 4203, Appli
Sequence 4204, Appli
Sequence 4205, Appli
Sequence 4206, Appli
Sequence 4365, Appli
Sequence 4366, Appli
Sequence 4367, Appli
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Sequence 4371, Appli
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Sequence 2193, Appli
Sequence 2305, Appli
Sequence 2306, Appli
Sequence 2307, Appli

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; GENERAL INFORMATION:
; TITLE OF INVENTION: Enhanced Secretion of a Polypeptide by a
; Microorganism
; FILE REFERENCE: GC636-2
; CURRENT APPLICATION NUMBER: US/09/975,132A
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/239,531
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO: 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: synthetic peptide tag
; OTHER INFORMATION: Peptide for generating antibodies
US-10-080-866-19

Query Match 72.7%; Score 8; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-10-037-243-3
; Sequence 3, Application US/10037243
; Publication No. US2003014352A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates, Inc.
; ATTORNEY: Freimuth, Paul I
; ATTORNEY: Zhang, Yian-Biao
; ATTORNEY: Howitt, Jason A
; TITLE OF INVENTION: Facilitating Protein Folding and Solubility by Use of Peptide Ext:
; FILE REFERENCE: BSA 01-22
; CURRENT APPLICATION NUMBER: US/10/037,243
; CURRENT FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic recognition motif
US-10-037-243-3

Query Match 54.5%; Score 6; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-09-983-802-398
; Sequence 398, Application US/09983802
; Publication No. US20030022185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

RESULT 4
US-10-080-866-19
; Sequence 19, Application US/10080866
; Publication No. US20030109024A1
; GENERAL INFORMATION:
; APPLICANT: Paegle, E. Sasha
; APPLICANT: Reilly, Dorothy
; APPLICANT: Yanbuia, Daniel C.
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1733R1
; CURRENT APPLICATION NUMBER: US/10/080,866

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PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
 PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
 PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
 PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
 NUMBER OF SEQ ID NOS: 672
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 398
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-984-490-398

Query Match 45.5%; Score 5; DB 10; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10
 Db 14 NYAAA 18

RESULT 8
 US-09-973-278-508
 Sequence 508, Application US/00973278
 Publication No. US20040044191A1
 GENERAL INFORMATION:
 APPLICANT: Fischer et al.
 TITLE OF INVENTION: 123 Human Secreted Proteins
 FILE REFERENCE: PZ01OP2
 CURRENT FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: 60/239,899
 PRIOR FILING DATE: 2000-10-13
 PRIOR APPLICATION NUMBER: 09/227,357
 PRIOR FILING DATE: 1999-01-08
 PRIOR APPLICATION NUMBER: US/09/973,278
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/051,926
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/052,793
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,925
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,929
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/052,803
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/052,732
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,931
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,932
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,916
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,930
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,918
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,920
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/052,733
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/052,795
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,919
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/051,928
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/055,722

PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,723
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,948
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,949
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,953
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,950
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,947
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,964
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/056,360
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,684
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,984
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/055,954
 PRIOR FILING DATE: 1997-08-18
 PRIOR APPLICATION NUMBER: 60/058,785
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: 60/058,664
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: 60/058,560
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: 60/058,661
 PRIOR FILING DATE: 1997-09-12
 NUMBER OF SEQ ID NOS: 947
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 508
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-973-278-508

Query Match 45.5%; Score 5; DB 11; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 6 NYAAA 10
 Db 14 NYAAA 18

RESULT 9
 US-10-895-372-316
 Sequence 316, Application US/10895372
 Publication No. US20050032705A1
 GENERAL INFORMATION:
 APPLICANT: Watkins, Maren
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: Hilliard, David R.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Jones, Robert M.
 TITLE OF INVENTION: Alpha-Comotoxin Peptides
 FILE REFERENCE: 2314-286
 CURRENT APPLICATION NUMBER: US/10/895,372
 CURRENT FILING DATE: 2004-07-21
 PRIOR FILING DATE: 2000-01-28
 PRIOR APPLICATION NUMBER: US 09/493,795
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: US 60/118,381
 NUMBER OF SEQ ID NOS: 404
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 316
 LENGTH: 41
 TYPE: PRT
 ORGANISM: Conus catcus
 US-10-895-372-316

Query Match Score 5; DB 17; Length 41;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDE 5
 Db 7 AANDE 11

RESULT 10
 US-09-837-537B-1
 Sequence 1; Application US/09837537B
 Publication No. US20020061839A1
 GENERAL INFORMATION:
 APPLICANT: SCHARPE, Simon Lodewijk
 DE MEESTER, Ingrid Anna Jozef
 APPLICANT: BELIAEV, Alexandre Arkadievitch
 APPLICANT: LAMBEIR, Anne-Marie Virginie Renee
 APPLICANT: AUGUSTYNIS, Koen Jan Iudovicus
 APPLICANT: HAEMERS, Achiel Jean-Marie
 APPLICANT: GOOSSENS, Dirk Frans
 TITLE OF INVENTION: Serine Peptidase Modulators
 FILE REFERENCE: 702 010673
 CURRENT APPLICATION NUMBER: US/09/837,537B
 CURRENT FILING DATE: 2001-04-18
 PRIOR APPLICATION NUMBER: EP 98200733 . 8
 PRIOR FILING DATE: 1998-03-09
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: MS Word 97 SR-2
 SEQ ID NO 1
 LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Functional group linked by Suc and MeO to phosphorus atom
 OTHER INFORMATION: Functional group linked by Suc and MeO to phosphorus atom
 OTHER INFORMATION: in serine peptidase/protease modulating compound
 US-09-837-537B-1

Query Match Score 4; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAY 11
 Db 1 AAAV 4

RESULT 11
 US-10-427-208-17
 Sequence 17; Application US/10427208
 Publication No. US20030200555A1
 GENERAL INFORMATION:
 APPLICANT: Merck & Co., Inc.
 APPLICANT: Hazuda, Daria J.
 APPLICANT: Chen Dodson, Elizabeth
 APPLICANT: Lai, Ming-Tain
 APPLICANT: Xu, Min
 APPLICANT: Shi, Xiao-Ping
 APPLICANT: Simon, Adam J.
 APPLICANT: Wu, Guoxin
 APPLICANT: Li, Xueming
 APPLICANT: Register, Robert B.
 TITLE OF INVENTION: ASSAYS USING AMYLOID PRECURSOR PROTEINS WITH MODIFIED
 TITLE OF INVENTION: BETA-SECRETASE CLEAVAGE SITES TO MONITOR BETA-SECRETASE ACTIVITY
 FILE REFERENCE: 21052
 CURRENT APPLICATION NUMBER: US/10/427,208
 CURRENT FILING DATE: 2003-04-30
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 17
 LENGTH: 4

Query Match Score 4; DB 15; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAA 9
 Db 1 NYAA 4

RESULT 12
 US-09-991-262-25
 Sequence 25; Application US/09991262
 Publication No. US20030041349A1
 GENERAL INFORMATION:
 APPLICANT: Christian, P. D.; Gordon, K. H.J.; Hanzlik, T. N.
 TITLE OF INVENTION: Novel sequence of known enzyme cleavage site
 OTHER INFORMATION: novel sequence of known enzyme cleavage site
 US-10-427-208-17

Query Match Score 4; DB 15; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAA 9
 Db 1 NYAA 4

NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flier Hohbach Test Albritton & Herbert LLP
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/991-262
 FILING DATE: 20-No. US20030041349A1-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/234,238
 FILING DATE: 20-JAN-1999
 APPLICATION NUMBER: US 09/485,355
 FILING DATE: 07-JUN-1995
 APPLICATION NUMBER: US 08/440,522
 FILING DATE: 12-MAY-1995
 APPLICATION NUMBER: US 08/089,372
 FILING DATE: 08-JUL-1993
 APPLICATION NUMBER: AU P4081/92
 FILING DATE: 14-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Trecartin, Richard P.
 REGISTRATION NUMBER: 31,801
 REFERENCE/DOCKET NUMBER: A-58631-3/RFT/DSS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEX: 910 27729
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:
 US-09-991-262-25

Query Match Score 4; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      8 AAAV 11
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Db      2 AAIV 5

RESULT 13
US-10-007-761-30
; Sequence 30, Application US/10007761
; GENERAL INFORMATION:
;   APPLICANT: Mochly-Rosen, Daria
;   TITLE OF INVENTION: Peptides For Activation and Inhibition
;   TITLE OF INVENTION: Of delta-PKC
;   FILE REFERENCE: 58630-8208 US00
;   CURRENT APPLICATION NUMBER: US/10/007,761
;   CURRENT FILING DATE: 2001-11-09
;   PRIOR APPLICATION NUMBER: US 60/262,060
;   PRIOR FILING DATE: 2001-01-18
;   NUMBER OF SEQ ID NOS: 72
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO: 30
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-delta RACK peptide
US-10-007-761-30

Query Match          36.4%; Score 4; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 AND 4
      |||||
Db      3 AAND 6

RESULT 14
US-10-435-608-27
; Sequence 27, Application US/10435608
; GENERAL INFORMATION:
;   APPLICANT: Blumberg, Richard S.
;   APPLICANT: Lencer, Wayne I.
;   APPLICANT: Simister, Neil E.
;   APPLICANT: Bionti, Alan J.
;   TITLE OF INVENTION: CENTRAL AIRWAY ADMINISTRATION FOR SYSTEMIC DELIVERY OF THERAPEUTIC
;   FILE REFERENCE: S01383.70010.US
;   CURRENT APPLICATION NUMBER: US/10/435,608
;   CURRENT FILING DATE: 2003-05-09
;   PRIOR APPLICATION NUMBER: PCT/US02/21335
;   PRIOR FILING DATE: 2002-07-03
;   PRIOR APPLICATION NUMBER: US 60/364,482
;   PRIOR FILING DATE: 2002-03-15
;   NUMBER OF SEQ ID NOS: 27
;   SOFTWARE: PatentIn version 3.1
SEQ ID NO: 27
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligopeptide
US-10-435-608-27

Query Match          36.4%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      8 AAAV 11
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Db      5 AAAV 8

Search completed: May 5, 2005, 18:31:03
Job time : 79 secs

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Scoring table:	OLIGO	Q9UC79	PRELIMINARY;	PRT;	26 AA.
GapOp:	60.0				
Searched:	1612378 seqs, 512079187 residues				
Word size :	0				
Total number of hits satisfying chosen parameters:	68540				
Minimum DB seq length: 0					
Maximum DB seq length: 50					
Post-processing: Listing first 45 summaries					
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
Result No.	Score	Query Match	Description		
Result No.	Score	Match	Length	DB	ID
1	8	72.7	26	O9UC79	
2	7	63.6	10	P96306	Q9uc79 homo sapien
3	7	63.6	10	P96321	p96306 escherichia
4	7	63.6	10	P96352	p96321 escherichia
5	7	63.6	10	P921ES	P96352 marinobacte
6	5	45.5	14	P96350	Q931ES photobacter
7	5	45.5	15	Q9UWH6	P96350 legionella
8	5	45.5	22	Q9UWHS	Q9uw6 thermococcus
9	5	45.5	30	Q95C4	Q9uw5 pyrococcus
10	4	36.4	8	Q7m3L7	Q9rc54 comamonas.
11	4	36.4	10	P96421	Q7m3L7 ascidiae cer
12	4	36.4	12	Q9EB19	P96421 neisseria g
13	4	36.4	12	Q9BOV3	Q9eb19 sus scrofa
14	4	36.4	15	Q47893	Q9eqv3 mus musculus
15	4	36.4	17	Q7qAV8	Q47893 frenyella d
16	4	36.4	18	O64353	Q7qav8 escherichia
17	4	36.4	19	Q9UR67	O64353 bacterioph
18	4	36.4	19	Q99MN2	Q9ur67 aspergillus
19	4	36.4	19	Q9396	Q99mn2 rattus norve
20	4	36.4	20	TLP_ACTRH	Q9396 swine herpes
21	4	36.4	20	Q9341	P83958 actinidia c
22	4	36.4	20	Q9RD9	Q29341 sus scrofa
23	4	36.4	20	Q9AW46	Q9rd9 escherichia
24	4	36.4	22	QDN6J2	Q9aw46 brachydano
25	4	36.4	22	Q9NDS9	Qdn6j2 balanus amp
26	4	36.4	22	Q9NDT8	Q9nds9 balanus amp
27	4	36.4	22	Q95P13	Q9ndt8 balanus amp
28	4	36.4	22	Q85515	Q95p13 chlamydia t
29	4	36.4	22	Q9R4W9	Q85515 chlamydia t
30	4	36.4	22	Q87084	Q9r4w9 burkholderi
31	4	36.4	22	Q87085	Q87084 swine herpes

RL	RNA 2:1306-1310(1996).	DR	EMBL; U68075; AAB48022..1; -.	
DR	NON TER 1 1	FT	U58075; AAB48022..1;	
FT	SEQUENCE . 10 AA; 1051 MW;	SQ	857BD22DCB544B1A CRC64;	
Query Match	Score 7; DB 2; Length 10;	Query Match	Score 6%; Best Local Similarity 100.0%; Pred. No. 1.2;	
Best Local Similarity 100.0%; Pred. No. 1.2;	Matches 7; Conservative 0; Mismatches 0;	Matches 7; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;	
Qy	2 ANDENYA 8	Qy	2 ANDENYA 8	
Db	1 ANDENYA 7	Db	1 ANDENYA 7	
RESULT 3	P96321 PRELIMINARY; PRT; 10 AA.	RESULT 5	P96325 PRELIMINARY; PRT; 10 AA.	
ID P96321;	AC P96321;	ID Q93LE5	AC Q93LE5;	
AC P96321;	PRELIMINARY;	ID Q93LE5;	PRELIMINARY;	
DT 01-MAY-1997 (TREMBLrel. 03, Created)	DT 01-DEC-2001 (TREMBLrel. 19, Created)	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)	DE Proteolysis tag (Fragment).	DE Proteolysis tag (Fragment).	OS Photobacterium phosphoreum.	
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)	DE Coded portion of Proteolysis tag (Fragment).	OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;	OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;	
DE Coded portion of Proteolysis tag (Fragment).	OS Escherichia coli.	OC Vibionaceae; Photobacterium.	OC Vibionaceae; Photobacterium.	
OS Escherichia coli.	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	NCBI_TaxID=562;	NCBI_TaxID=659;	
OC Enterobacteriaceae; Escherichia.	OX [1]	RN [1]	RN [1]	
OX [1]	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	
RP SEQUENCE FROM N.A.	RX MEDLINE=20063247; PubMed=10592213; DOI=10.1093/nar/28.1.168;	RX MEDLINE=20063247; PubMed=10592213; DOI=10.1093/nar/28.1.168;	RX MEDLINE=20063247; PubMed=10592213; DOI=10.1093/nar/28.1.168;	
STRAIN=ATCC 133;	RA Williams K.P.;	RA Williams K.P.;	RA Williams K.P.;	
RX MEDLINE=97128184; PubMed=8927778;	RA Williams K.P.;	RA Williams K.P.;	RA Williams K.P.;	
RA Williams K.P., Bartel D.P.;	RT "The tmRNA website."	RT "The tmRNA website."	RT "The tmRNA website."	
RT "Phylogenetic analysis of tmRNA secondary structure.";	RL Nucleic Acids Res. 28:168-168 (2000).	RL Nucleic Acids Res. 28:168-168 (2000).	RL Nucleic Acids Res. 28:168-168 (2000).	
RL 2:1306-1310(1996).	RN [2]	RN [2]	RN [2]	
RN [2]	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	
SEQUENCE FROM N.A.	RX Submitted (JUN-2001) to the EMBL/GenBank/DBJ database.	RX Submitted (JUN-2001) to the EMBL/GenBank/DBJ database.	RX Submitted (JUN-2001) to the EMBL/GenBank/DBJ database.	
RC STRAIN=ATCC 133.	RA Williams K.P.;	RA Williams K.P.;	RA Williams K.P.;	
RX MEDLINE=97128184; PubMed=8927778;	RA Williams K.P.;	RA Williams K.P.;	RA Williams K.P.;	
RA Williams K.P., Bartel D.P.;	RT "Phylogenetic analysis of tmRNA secondary structure.";	RT "Phylogenetic analysis of tmRNA secondary structure.";	RT "Phylogenetic analysis of tmRNA secondary structure.";	
RT "A tmRNA-like structure is present in 10S rRNA, a small stable RNA from Escherichia coli.";	RL Nucleic Acids Res. 28:168-168 (2000).	RL Nucleic Acids Res. 28:168-168 (2000).	RL Nucleic Acids Res. 28:168-168 (2000).	
RA Komine Y., Kitabayashi M., Yokogawa T., Nishikawa K., Inokuchi H.;	RA Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).	RA Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).	RA Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).	
RT Escherichia coli.	DR U68074; AAB48024..1; -.	DR U68074; AAB48024..1; -.	DR U68074; AAB48024..1; -.	
NON TER 1 1	FT 1 1	FT 1 1	FT 1 1	
SEQUENCE 10 AA; 1051 MW;	SQ 857BD22DCB544B1A CRC64;	SQ 857BD22DCB544B1A CRC64;	SQ 857BD22DCB544B1A CRC64;	
Query Match	Score 7; DB 2; Length 10;	Query Match	Score 7; DB 2; Length 10;	
Best Local Similarity 100.0%; Pred. No. 1.2;	Matches 7; Conservative 0; Mismatches 0;	Best Local Similarity 100.0%; Pred. No. 1.2;	Matches 7; Conservative 0; Mismatches 0;	
Matches 7; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;	Indels 0; Gaps 0;	Indels 0; Gaps 0;	
Qy	2 ANDENYA 8	Qy	2 ANDENYA 8	
Db	1 ANDENYA 7	Db	1 ANDENYA 7	
RESULT 4	P96352 PRELIMINARY; PRT; 10 AA.	RESULT 6	P96350 PRELIMINARY; PRT; 14 AA.	
ID P96352;	AC P96352;	ID P96350	AC P96350;	
AC P96352;	PRELIMINARY;	ID P96350;	PRELIMINARY;	
DT 01-MAY-1997 (TREMBLrel. 03, Created)	DT 01-MAY-1997 (TREMBLrel. 03, Created)	DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)	DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)	
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)	DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DE Coded portion of Proteolysis tag (Fragment).	DE Coded portion of Proteolysis tag (Fragment).	DE Coded portion of Proteolysis tag (Fragment).	
DE Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).	OS Legionella pneumophila.	OS Legionella pneumophila.	OS Legionella pneumophila.	
DE Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).	OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;	OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;	OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;	NCBI_TaxID=2743;	NCBI_TaxID=446;	NCBI_TaxID=446;	
NCBI_TaxID=2743;	RN [1]	RN [1]	RN [1]	
RN [1]	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	
RP SEQUENCE FROM N.A.	RX MEDLINE=97128184; PubMed=8927778;	RX MEDLINE=97128184; PubMed=8927778;	RX MEDLINE=97128184; PubMed=8927778;	
RX MEDLINE=97128184; PubMed=8927778;	RA Williams K.P., Bartel D.P.;	RA Williams K.P., Bartel D.P.;	RA Williams K.P., Bartel D.P.;	
RA Williams K.P., Bartel D.P.;	RT "Phylogenetic analysis of tmRNA secondary structure.";	RT "Phylogenetic analysis of tmRNA secondary structure.";	RT "Phylogenetic analysis of tmRNA secondary structure.";	
RT "Phylogenetic analysis of tmRNA secondary structure.";	RL RNA 2:1306-1310(1996).	RL RNA 2:1306-1310(1996).	RL RNA 2:1306-1310(1996).	
RL RNA 2:1306-1310(1996).	DR U68079; AAB48026..1; -.	DR U68079; AAB48026..1; -.	DR U68079; AAB48026..1; -.	
DR U68079; AAB48026..1; -.	FT NON TER 1 1	FT NON TER 1 1	FT NON TER 1 1	
FT NON TER 1 1	SQ SEQUENCE 14 AA; 1349 MW;	SQ SEQUENCE 14 AA; 1349 MW;	SQ SEQUENCE 14 AA; 1349 MW;	
SQ SEQUENCE 14 AA; 1349 MW;	CBSF7310D3BE7DD CRC64;	CBSF7310D3BE7DD CRC64;	CBSF7310D3BE7DD CRC64;	
CBSF7310D3BE7DD CRC64;	Query Match	Score 5%; Best Local Similarity 100.0%;	Query Match	Score 5%; Best Local Similarity 100.0%;
Query Match	Length 14;	Length 14;	Length 14;	
Length 14;	Pred. No. 1.8e+02;	Pred. No. 1.8e+02;	Pred. No. 1.8e+02;	

Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	ID	Q9R5C4	PRELIMINARY;	PRT;	30 AA.
Qy	2 ANDEN 6 									AC	Q9R5C4;			
Db	1 ANDEN 5									DT	01-MAY-2000 (TREMBLrel. 13, Created)			
RESULT 7														
Q9UWH6		PRELIMINARY;		PRT;	15 AA.					RN	[1]			
AC	Q9UWH6;									RP				
DT	01-MAY-2000 (TREMBLrel. 13, Created)									SEQUENCE.				
DT	01-JUN-2000 (TREMBLrel. 13, Last sequence update)									RX	MEDLINE=93215645; PubMed=8462543;			
DB	Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha									RA	Ogawa J., Shimizu S., Yamada H.,			
DB	(Fragment).									RT	"N-carbamoyl-D-amino acid amidohydrolase from <i>Comamonas</i> sp. E222c			
OS	<i>Thermococcus litoralis</i> .									RT	purification and characterization";			
OC	Archaea; Euryarchaeota; Thermococci; Thermococcaceae;									RL	Eur. J. Biochem. 212:685-691 (1993).			
OC	<i>Thermococcus</i> .									SQ	SEQUENCE 30 AA; 3323 MW; CBA003DE1A22133F CRC64;			
OX	NCBI_TAXID=2265;									Query Match	45.5%; Score 5; DB 2; Length 30;			
RN	[1]									Best Local Similarity	100.0%; Pred. No. 3.5e-02;			
RP										Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
RX	MEDLINE=96146528; PubMed=8550513;									Qy	6 NYAA 10 5 NYAA 9			
RA	Heider J., Mai X., Adams M.W.;									Db				
RT	"Characterization of 2-ketosovalerate ferredoxin oxidoreductase, a new and reversible coenzyme A-dependent enzyme involved in peptide fermentation by hyperthermophilic archaea.";									RESULT 10	Q7M3L7	PRELIMINARY;	PRT;	8 AA.
RT	J. Bacteriol. 178:780-787(1996); SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;									ID	Q7M3L7	PRELIMINARY;	PRT;	8 AA.
SQ										AC	Q7M3L7;			
RESULT 8														
Q9UWH6		PRELIMINARY;		PRT;	22 AA.					RN	[1]			
AC	Q9UWH6;									RP				
DT	01-MAY-2000 (TREMBLrel. 13, Created)									SEQUENCE.				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)									RX	MEDLINE=96132650; PubMed=8554314; DOI=10.1006/abbi.1995.0035;			
DB	Keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha									RA	Taylor S.W., Ross M.M., Waite J.H.;			
DB	(Fragment).									RT	"Novel 3,4-dihydroxyphenylalanine-containing polypeptides from the blood cells of the ascidians <i>Ascidia ceratodes</i> and <i>Molgula manhattensis</i> ";			
OS	<i>Archaea; Euryarchaeota; Thermococci; Thermococcaceae;</i>									RL	Arch. Biochem. Biophys. 324:228-240 (1995).			
OC	<i>Pyrococcus</i> .									DR	PIR; S68325; S68325.			
OC	<i>Pyrococcus furiosus.</i>									FT	NON-TER 1 NON-TER 1 FT			
OC	<i>Pyrococcus.</i>									FT	8 AA; 907 MW; D9DDDDDCB4B4B5A CRC64;			
OX	NCBI_TAXID=2261;									SQ				
RN	[1]									Query Match	36.4%; Score 4; DB 2; Length 8;			
RP										Best Local Similarity	100.0%; Pred. No. 1.6e+06;			
RX	MEDLINE=96146528; PubMed=8550513;									Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
RA	Heider J., Mai X., Adams M.W.;									Qy	7 YAAA 10 4 YAAA 7			
RT	"Characterization of 2-ketosovalerate ferredoxin oxidoreductase, a new and reversible coenzyme A-dependent enzyme involved in peptide fermentation by hyperthermophilic archaea.";									Db				
RT	J. Bacteriol. 178:780-787(1996).									RESULT 11	P96421	PRELIMINARY;	PRT;	10 AA.
RL	SEQUENCE 22 AA; 2465 MW; 684CBA3E5D750A0D CRC64;									ID	P96421;			
SQ										AC	P96421;			
RESULT 9														
Q9R5C4		PRELIMINARY;		PRT;	22 AA.					DT	01-MAY-1997 (TREMBLrel. 03, Created)			
AC	Q9R5C4;									DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)									DT	01-MAR-1998 (TREMBLrel. 08, Last annotation update)			
DE	N-carbamoyl-D-amino acid amidohydrolase (Fragment).									DE	Coded portion of proteolysis tag (Fragment).			
OS	<i>Comamonas</i> .									OS	<i>Neisseria gonorrhoeae.</i>			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;									OC	<i>Neisseriaceae; Neisseria.</i>			

OX NCBI_TaxID=485;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=ATCC 19424; PubMed=11179961;
 RC MEDLINE=91128184; PubMed=8972778;
 RX Williams K.P.; Barriel D.P.;
 RT "Phylogenetic analysis of tRNA secondary structure.";
 RA RNA 2:1306-1310(1996).
 RL EMBL; U68080; AAB48028.1; -.
 DR NON_TER 1 1
 FT NON_TER 10 AA; 1038 MW; 857BD22DCB41AB1A CRC64;
 SQ SEQUENCE 10 AA; 1038 MW;

Query Match Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ANDE 5
 Db 1 ANDE 4

RESULT 12
 Q6EBI19 PRELIMINARY; PRT; 12 AA.
 ID Q6EBI19
 AC Q6EBI19; PRELIMINARY; PRT; 12 AA.
 DT 25-OCT-2004 (TREMBLrel. 28; Created)
 DT 25-OCT-2004 (TREMBLrel. 28; Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28; Last annotation update)
 DE CAMK1-like protein kinase (Fragment).
 OS Sus scrofa (Pig).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 NCBI_TaxID=9823;
 RN [1] SEQUENCE FROM N.A.
 RP Nonneman D.; Rohrer G.A.;
 RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RT "Comparative mapping of human chromosome 10 to pig chromosomes 10 and
 14.";
 RT Anim. Genet. 35:338-343 (2004).
 RN [2] SEQUENCE FROM N.A.
 RP Nonneman D.J.; Rohrer G.A.;
 RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY668181; AR243861;
 GO; GO:0016301; PKinase activity; IFA.
 KW Kinase.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1259 MW; CF317FF387CDDDD CRC64;

Query Match Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAV 11
 Db 5 AAAV 8

RESULT 13
 Q9EQV3 PRELIMINARY; PRT; 12 AA.
 ID Q9EQV3
 AC Q9EQV3; PRELIMINARY; PRT; 12 AA.
 DT 01-MAR-2001 (TREMBLrel. 16; Created)
 DT 01-DEC-2001 (TREMBLrel. 16; Last sequence update)
 DE Alpha-sarcoglycan (Fragment).
 GN Name=sgrca;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 RX MEDLINE=2109368; PubMed=11179961;
 RA Wakabayashi-Takai E.; Noguchi S.; Ozawa E.;
 RT "Identification of myogenesis-dependent transcriptional enhancers in
 promoter region of mouse gamma-barrcoglycan gene.";
 RL Biochem. 268:948-957(2001).
 DR EMBL; AB044625; BAB18770.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1257 MW; D382726D594361B2 CRC64;

Query Match Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAV 11
 Db 2 AAAV 5

RESULT 14
 Q47893 PRELIMINARY; PRT; 15 AA.
 ID Q47893
 AC Q47893; PRELIMINARY; PRT; 15 AA.
 DT 01-NOV-1996 (TREMBLrel. 01; Created)
 DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)
 DE Beta-phycocyanin (Fragment).
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae;
 NCBI_TaxID=1197;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=86233345; PubMed=3086870;
 RA Conley P.B.; Lemieux P.G.; Lomax T.L.; Grossman A.R.;
 RT "Genes encoding major light-harvesting polypeptides are clustered on
 the genome of the cyanobacterium Fremyella diplosiphon.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
 DR EMBL; M13217; AAA24880.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1528 MW; 7FFF2F65518F493D4 CRC64;

Query Match Score 4; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AAAV 11
 Db 11 AAAV 14

RESULT 15
 Q79AV8 PRELIMINARY; PRT; 17 AA.
 ID Q79AV8
 AC Q79AV8; PRELIMINARY; PRT; 17 AA.
 DT 05-JUL-2004 (TREMBLrel. 27; Created)
 DT 05-JUL-2004 (TREMBLrel. 27; Last sequence update)
 DE Gene malG for maltose transport (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 NCBI_TaxID=52;

RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=86081738; PubMed=3000770;
 RX
 RA Dassa E.; Hornung M.;
 RT "Sequence of gene malG in E. coli K12: homologies between integral
 membrane components from binding protein-dependent transport
 systems.";
 RL EMBL J. 4:2287-2293 (1985).
 DR EMBL; X02871; CAA26629.1; -.
 FT NON_TER 17 17

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SQ  SEQUENCE  17 AA;  1878 MW;  E6C439F48AB27EED CRC64;  
Query Match 36.4%;  Score 4;  DB 2;  Length 17;  
Best Local Similarity 100.0%;  Pred. No. 2.2e+03;  
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;  
Qy 7 YAAA 10  
    ||||  
Db 7 YAAA 10
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Job time : 95.3333 sec_B

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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:10:34 ; Search time 20.3333 Seconds
(without alignments)

52.052 Million cell updates/sec

Title: US-10-827-133-8

Perfect score: 11

Sequence: 1 AANDENYAAAV 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : PIR_79;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	45.5	30	2 S30333	N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.-.-) - Comamonas sp. (fragment)
2	4	36.4	8	2 S66325	N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.-.-) - Comamonas sp.
3	4	36.4	18	2 T13132	C;Species: Comamonas sp.
4	4	36.4	24	2 A24802	C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 26-May-2000
5	4	36.4	25	2 A61148	A;Title: N-carbamoyl-D-amino acid amidohydrolase from Comamonas sp. E222c. Purification
6	4	36.4	27	2 S05219	A;Reference number: S30333; MUID: 8462543; PMID: 8462543
7	4	36.4	28	2 E81239	A;Molecule type: Protein
8	4	36.4	30	2 I39199	C;Keywords: hydrolyase
9	4	36.4	30	2 B47607	RESULT 1
10	4	36.4	32	2 F60529	S30333 N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.-.-) - Comamonas sp. (fragment)
11	4	36.4	34	2 PC13139	C;Species: Comamonas sp.
12	4	36.4	34	2 A87279	C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
13	4	36.4	36	2 C84175	C;Accession: S66325
14	4	36.4	37	2 A32000	A;Residues: 1-8 <TAY>
15	4	36.4	37	2 S17684	A;Cross-references: UNIPROT:Q7M3L7
16	4	36.4	37	2 C84210	F;2, 4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental
17	4	36.4	37	2 AH2787	A;Title: Novel 3',4-di- and 3',5-trihydroxyphenylalanine-containing polypeptides from th
18	4	36.4	38	2 S07140	A;Reference number: S68325; MUID: 96132650; PMID: 8554314
19	4	36.4	38	2 H95005	A;Accession: S68325
20	4	36.4	38	2 G81904	A;Molecule type: Protein
21	4	36.4	39	2 AB0930	C;Residues: 1-8 <TAY>
22	4	36.4	39	2 AF0836	A;Cross-references: UNIPROT:Q7M3L7
23	4	36.4	41	2 S00776	F;2, 4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental
24	4	36.4	41	2 E82544	A;Title: Novel 3',4-di- and 3',5-trihydroxyphenylalanine-containing polypeptides from th
25	4	36.4	42	2 D37416	A;Reference number: S68325; MUID: 96132650; PMID: 8554314
26	4	36.4	44	1 BX2A1	A;Accession: S68325
27	4	36.4	45	2 PN0590	A;Cross-references: UNIPROT:Q7M3L7
28	4	36.4	45	2 PN0589	F;2, 4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental
29	4	36.4	45	2 B40432	A;Title: Novel 3',4-di- and 3',5-trihydroxyphenylalanine-containing polypeptides from th

ALIGNMENTS

RESULT 1

S30333 N-carbamoyl-D-amino acid amidohydrolase (EC 3.5.-.-) - Comamonas sp.

C;Species: Comamonas sp.

C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 26-May-2000

C;Accession: S30333

R;Ogawa, J.; Shimizu, S.; Yamada, H.
Bur. J. Biochem. 212, 685-691, 1993

A;Title: N-carbamoyl-D-amino acid amidohydrolase from Comamonas sp. E222c. Purification

A;Reference number: S30333; MUID: 8462543; PMID: 8462543

A;Molecule type: Protein

A;Keywords: hydrolyase

Query Match 45.5%; Score 5; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10

Db 5 NYAAA 9

RESULT 2

S66325 blood cell protein A8 - Ascidia ceratodes (fragment)

N;Alternative names: Abcp-A

C;Species: Ascidia ceratodes

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C;Accession: S66325

R;Taylor, S.W.; Ross, M.M.; White, J.H.
Arch. Biochem. Biophys. 324, 228-240, 1995

A;Title: Novel 3',4-di- and 3',5-trihydroxyphenylalanine-containing polypeptides from th

A;Reference number: S68325; MUID: 96132650; PMID: 8554314

A;Accession: S68325

A;Molecule type: Protein

A;Residues: 1-8 <TAY>

A;Cross-references: UNIPROT:Q7M3L7

F;2, 4/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental

Query Match 36.4%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YAAA 10

|||||

C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I39799
 R;Duvall, E.J.; Williams, D.M.; Mongolsuk, S.; Lovett, P.S.
 J;Bacteriol. 158, 788-790, 1984
 A;Title: Regulatory regions that control expression of two chloramphenicol-inducible cat
 A;Reference number: 139799; MUID:84212298; PMID:6327638
 A;Accession: I39799
 A;Status: Preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-30 <RES>
 A;Cross-references: UNIPROT:Q45356; GB:X01811; NID:9142647; PIDN:AAA22292.1; PID:9551696
 C;Superfamily: chloramphenicol acetyltransferase

Query Match	36.4%;	Score 4;	DB 2;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 7.6e+02;	Indels 0;	Gaps 0;
Matches	4;	Conservative 0;	Mismatches 0;	
Qy	4 DENY 7 Db	6 DENY 9		

RESULT 9
 B47607
 Immunogenic protein MPB70/MPB80 - Mycobacterium bovis (strain BCG) (fragment)
 C;Species: Mycobacterium bovis
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C;Accession: B47607
 R;Harboe, M.; Nagai, S.; Patarroyo, M.E.; Torres, M.L.; Cruz, N.
 Infect. Immun. 52, 233-302, 1986
 A;Title: Properties of proteins MPB64, MPB70, and MPB80 of Mycobacterium bovis BCG.
 A;Reference number: A47607; MUID:86166829; PMID:3514457
 A;Accession: B47607
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-30 <HAR>

Query Match	36.4%;	Score 4;	DB 2;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 7.6e+02;	Indels 0;	Gaps 0;
Matches	4;	Conservative 0;	Mismatches 0;	
Qy	7 YAAA 10 Db	11 YAAA 14		

RESULT 10
 F60529
 hemocyanin M1 - crayfish (*Cherax destructor*) (fragment)
 C;Species: Cherax destructor (yabby)
 C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 11-May-2000
 C;Accession: F60529
 R;Neureboom, B.; Sierdsma, S.J.; Beintema, J.J.
 Comp. Biochem. Physiol. B 94, 587-592, 1989
 A;Title: The relationship between N-terminal sequences and immunological characterization
 A;Reference number: A60529; MUID:90151075; PMID:2620501
 A;Accession: F60529
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-32 <NEU>

Query Match	36.4%;	Score 4;	DB 2;	Length 32;
Best Local Similarity	100.0%;	Pred. No. 8e+02;	Indels 0;	Gaps 0;
Matches	4;	Conservative 0;	Mismatches 0;	
Qy	3 NDEN 6 Db	27 NDEN 30		

RESULT 11
 PC1319
 large granule L9 chain - horseshoe crab (*Tachypleus tridentatus*) (fragment)

	Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	8	AAAV 11								
Db	16	AAAV 19								

RESULT 14

A32000 somatostatin, pancreatic - sea lamprey
 C;Species: Petromyzon marinus (sea lamprey)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C;Accession: A32000
 R; Andrews, P.C.; Pollock, H.G.; Elliott, W.M.; Youson, J.H.; Plisetskaya, E.M.
 J. Biol. Chem. 261, 15809-15814, 1988
 A;Title: Isolation and characterization of a variant somatostatin-14 and two related somatostatin-13 peptides from the lamprey Petromyzon marinus
 A;Reference number: A32000; MUID:89008497; PMID:2902094
 A;Accession: A32000
 A;Molecule type: Protein
 A;Residues: 1-37 <AND>
 A;Cross-references: UNIPROT:P21779
 C;Superfamily: Somatosatrin
 C;Keywords: neuropeptide

	Query Match	Score 4;	DB 2;	Length 37;
Best Local Similarity	100.0%	Pred. No. 9e+02;		
Matches	4;	Mismatches 0;		
		Indels 0;		
		Gaps 0;		

Qy 8 AAAV 11
 Db 4 AAAV 7

RESULT 15

S17684 thaumatin homolog 2 - barley
 C;Species: Hordeum vulgare (barley)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S17684
 R;Højgaard, J.; Jacobsen, S.; Svendsen, I.
 FEBS Lett. 291, 127-131, 1991
 A;Title: Two antifungal thaumatin-like proteins from barley grain.
 A;Reference number: S17573; MUID:92037994; PMID:1936240
 A;Accession: S17684
 A;Status: preliminary
 A;Molecule type: Protein
 A;Residues: 1-37 <HEJ>
 A;Cross-references: UNIPROT:P33045
 C;Superfamily: thaumatin I

	Query Match	Score 4;	DB 2;	Length 37;
Best Local Similarity	100.0%	Pred. No. 9e+02;		
Matches	4;	Mismatches 0;		
		Indels 0;		
		Gaps 0;		

Qy 8 AAAV 11
 Db 15 AAAV 18

Search completed: May 5, 2005, 18:25:28
 Job time : 23.3333 secs

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OM protein - protein search, using sw model

Run on: May 5, 2005, 18:00:34 ; Search time 101.333 Seconds
(without alignments)

41.984 Million cell updates/sec

Title: US-10-827-133-8

Perfect score: 11

Sequence: 1 AANDENYAAAV 11

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 938430

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :	A_Geneseq_16Dec04:
1:	GeneseqP19808:*
2:	GeneseqP19908:*
3:	GeneseqP20008:*
4:	GeneseqP20018:*
5:	GeneseqP20028:*
6:	GeneseqP20038:*
7:	GeneseqP2003bs:*
8:	GeneseqP20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	8	72.7	11	2	ABB84403	Abb84403 E. coli d
2	8	72.7	11	6	AAO16101	Aao16101 C-terminal
3	8	72.7	11	7	ADE18279	Ade48279 TAT depe
4	8	72.7	11	7	ADP50155	Adp50155 S. enteri
5	8	72.7	12	5	AAE28994	Aae28994 Peptid e u
6	6	54.5	6	5	ADL33753	Adl33753 Bacteriop
7	5	45.5	9	8	ADN633606	Adn633606 HLA bindi
8	5	45.5	14	7	ADD23307	Add23307 Breast ca
9	5	45.5	21	8	ADK50911	Adk50911 Human C35
10	5	45.5	22	7	ADC3576	Fusion pe
11	5	45.5	30	2	ABR37123	Abr37123 Decarboxy
12	5	45.5	31	7	ADA07577	Ada07577 Human sec
13	5	45.5	31	8	ADN1386	Novel hum
14	5	45.5	32	4	AAB61562	Aab61562 Peptid e W
15	5	45.5	32	4	AAB61569	Aab61569 Peptid e W
16	5	45.5	32	4	AAB61568	Aab61568 Peptid e W
17	5	45.5	32	4	AAB61559	Aab61559 Peptid e W
18	5	45.5	33	8	ADK50912	Adk50912 Human C35
19	5	45.5	37	4	AAB61571	Aab61571 Peptid e W
20	5	45.5	41	2	AY33241	Aay33241 Human bet
21	5	45.5	41	3	AAB21594	Aab21594 Cone snai
22	4	36.4	4	2	AAR55338	Aar55338 Inhibitor
23	4	36.4	4	4	AM52602	Aam52602 Serine pr
24	4	36.4	4	4	AAB97630	Aab97630 Elastase
25	4	36.4	5	2	AAR12715	Aar12715 Pentapept

ALIGNMENTS

RESULT 1
ABB84403 standard; peptide; 11 AA.

ID ABB84403
XX AC ABB84403;
XX DT 21-OCT-2002 (first entry)
XX DE E. coli derived aberrant protein C-terminal peptide motif.
XX KW Tumour antigen; murine; vaccine; cellular immune response; immunogen;
KW cancer; tumour.
XX OS Escherichia coli.

XX US6287569-B1.
XX PD 11-SEP-2001.
XX PF 06-APR-1998;
XX PF 06-APR-1998; 98US-00056105.
XX PR 10-APR-1997; 97US-0043467P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Kipps TJ, Wu Y;
XX DR WPI; 1998-583198/49.

Generating cellular immune response in patient to target protein - comprising introducing vector with nucleotide sequence encoding immunogen comprising protein processing signal into cell of patient.

Example 5; Col 6; 61pp; English.

This invention describes a novel method for generating a cellular immune response in a patient to a target protein or its fragment. The method involves introducing a vector containing a nucleotide sequence encoding a chimeric immunogen comprising a protein processing signal and the target protein or its fragment. The immunogen is produced by the cells and processed so that the target protein or its fragment is presented to the patients immune system and a cellular immune response is initiated. The method and vectors can be used as a form of vaccination and could be used to generate a cellular immune response in patients to, e.g. cancerous tumours. The cellular immune response is the predominant immune response in the patient. This sequence represents an E. coli aberrant protein motif described in the method of the invention. Note: The information in this spec has been previously disclosed in WO19985444 however this spec

CC contained no sequence information
 XX Sequence 11 AA;

Query Match 72.7%; Score 8; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
 | | | | |
 Db 1 AANDENYA 8

RESULT 2
 ID AAO16101 standard; peptide; 11 AA.
 XX AAO16101;
 AC AAO16101;
 DT 27-FEB-2003 (first entry)
 XX C-terminal tag peptide.
 DE Gene therapy; vaccine; humoral immune response; cellular immune response;
 KW immune response modulation; pathogenic infection; rheumatoid arthritis.
 OS Unidentified.
 XX WO200283181-A1.
 PN 24-OCT-2002.
 PD 18-APR-2002; 2002WO-AU000486.
 PR 18-APR-2001; 2001AU-00004468.
 PA (UQQU) UNIV QUEENSLAND.
 PI Frazer IH;
 XX WPI; 2003-075509/07.

PS New compositions having antigens, polynucleotides encoding the antigens, or antigen-presenting cells, useful for modulating an immune response, e.g., for treating or preventing pathogenic infections or rheumatoid arthritis.

PS Disclosure; Page 35; 139pp; English.

XX The invention comprises compositions for eliciting a humoral or cellular immune response against a target antigen. The compositions of the invention are useful for eliciting a humoral and cellular immune response against a target antigen, modulating an immune response in a patient, and the treatment or prophylaxis of a disease or condition. This includes pathogenic infections (e.g. viral, bacterial, fungal or protozoan), or an immune response to an autoantigen (e.g. rheumatoid arthritis). The present amino acid sequence represents a peptide which was used in the invention

XX Sequence 11 AA;

XX Query Match 72.7%; Score 8; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
 | | | | |
 Db 1 AANDENYA 8

RESULT 3
 ID ADE48279 standard; peptide; 11 AA.

XX ADE48279;
 AC XX DT 29-JAN-2004 (first entry)
 DE TAT dependant secretion clone #1.
 KW leader peptide; Twin Arginine Translocation pathway;
 KW putative TAT leader peptide sequence.
 OS Synthetic.
 XX PN WO2003040335-A2.

XX 15-MAY-2003.
 PD XX 05-NOV-2002; 2002WO-US035618.
 PR XX 05-NOV-2001; 2001US-0337451P.
 PR 21-AUG-2002; 2002US-0337452P.
 XX (RERE-) RES DEV FOUND.
 PA XX PI Georgiou G, Delisa M;
 XX DR WPI; 2003-449453/42.

XX Identifying a leader peptide that directs increased protein export in bacteria by screening libraries of leader peptides for sequences that allow rapid export and can rescue short-lived reporter protein from degradation in cytoplasm.

XX Example 7; SEQ ID NO 119; 63pp; English.

XX The present sequence relates to identifying a leader peptide that directs increased protein export in bacteria, optionally through the Twin Arginine Translocation pathway, comprises screening of libraries of putative leader peptides or their mutants for sequences that allow rapid export and, thus, can rescue a short-lived reporter protein from degradation in the cytoplasm. The method is useful in engineering of leader peptides for the secretion of recombinant proteins in bacteria. The leader peptides can be used to direct or enhance protein secretion. The present sequence represents a putative TAT leader peptide sequence of the invention.

XX Sequence 11 AA;

XX Query Match 72.7%; Score 8; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
 Db 1 AANDENYA 8

RESULT 4
 ID ADF50155 standard; peptide; 11 AA.
 XX ADF50155;
 AC XX DT 12-FEB-2004 (first entry)
 DE S. enteritidis protease C-terminal fragment.
 KW promoter; mutant; vaccine; Shine Dalgarno; probiotic bacteria;
 KW regulatory gene; targeted optimisation.
 XX OS Salmonella enteritidis.
 XX PN WO2003070941-A2.

RESULT 5
 ID ADF50155 standard; peptide; 11 AA.

PD 28-AUG-2003.
 XX WPI; 2002-723363/78.
 PF New vector comprising anti-termination nucleic acid or RNA encoding the
 XX PT polypeptide with a non-lambda promoter, useful for producing human
 PR thrombopoietin (TPO) or fibroblast growth factor-5 (FGF-5) polypeptide.
 XX PA Example 2; Page 32; 70pp; English.

PT Bumann D;
 XX DR 2003-712619/67.
 XX PT New bacterial promoters active in vivo, useful in preparation of live,
 PR recombinant vaccines, also mutated Shine-Dalgarno sequences for
 PT modulating promoter activity.
 XX PS Disclosure; SEQ ID NO 2; 92pp; German.
 XX CC This invention describes novel active promoters described as 4.5G, A.8H,
 CC 1F, 3g, 1c, 2a, 4a, 10g, 12b, A.2A, A.7A, A.9D, A.10F, A.11B, A.11H,
 CC A.12G, C.11C, C.11G, 3.9E, A.11A, A.8B, C.11.1C, C.11.1G, 3.2E,
 CC 3.6B, 3.9A, 3.9E, A.11A, A.8B, C.11.5N, 4.4G or A.1A and their mutants.
 CC The invention also describes recombinant bacteria that contains the
 CC promoter, operatively linked to a heterologous nucleic acid, live vaccine
 CC containing the bacteria and construct with mutations in the Shine
 CC Dalgarno sequence. The target bacteria are those used as carriers in live
 CC vaccines, particularly Salmonella or probiotic bacteria. The new
 CC promoters are used in preparation of live vaccines, especially for
 CC expression of heterologous antigen. Also the mutated Shine-Dalgarno
 CC sequence is used to modify (especially reduce) the activity of regulatory
 CC gene elements, for targeted optimisation of the properties of recombinant
 CC live vaccines. The new promoters (and/or mutated Shine-Dalgarno
 CC sequences) provide targeted modulation of gene expression, including,
 CC where the promoter has high activity both in vivo and in vitro induction
 CC of a two-phase immune response.
 XX Sequence 11 AA;

Query Match 72.7%; Score 8; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.096; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AANDENYA 8
 Db 1 AANDENYA 9

RESULT 6
 ADL33753 ID ADL33753 standard; protein; 6 AA.
 XX AC ADL33753;
 XX DT 20-MAY-2004 (first entry)
 XX DB Bacteriophage T7 ssrA peptide.
 XX KW protein solubility; coxsackievirus and adenovirus receptor; CAR;
 XX KW Bacteriophage T7; ssrA peptide.
 XX OS Enterobacteria phage T7.
 XX PN US2003134352-A1.
 XX PD 17-JUL-2003.
 XX PP 04-JAN-2002; 2002US-00037243.
 XX PR 04-JAN-2002; 2002US-00037243.

RESUL 5
 AAE28994 ID AAE28994 standard; peptide; 12 AA.
 XX AC AAE28994;
 XX DT 27-JAN-2003 (first entry)
 XX DB Peptide used in the exemplification of the invention.
 XX KW Vector; prokaryotic cell.
 XX OS Unidentified.
 PN WO200272847-A2.

XX PD 19-SEP-2002.
 XX PF 22-FEB-2002; 2002WO-US005069.
 XX PR 09-MAR-2001; 2001US-0274384P.
 XX PA (GETH) GENENTECH INC.
 PI Paegle ES, Reilly D, Yansura DG;

XX PS Disclosure; Page 9; 21pp; English.
 XX CC The invention relates to a method of enhancing the solubility of, and
 CC promoting the adoption of native protein conformation of a recombinantly
 CC expressed polypeptide by expressing the polypeptide as a fusion protein
 CC including a peptide extension with: net negative charge (not peptide T7A)
 CC positioned at the carboxyl terminus; or net charge +2 to -20, positioned
 CC at the amino terminus. The nucleic acids encoding the polypeptide of
 CC interest and the extension are fused and inserted into an expression
 CC vector which is then introduced into a host cell in which the polypeptide
 CC is produced. The polypeptide is especially one that is substantially

CC insoluble or inactive when expressed recombinantly without the peptide extension. The present sequence represents Bacteriophage T7 *ssrA* Peptide, used in a fusion to demonstrate the method of the invention.

XX Sequence 6 AA;
 SQ Query Match 54.5%; Score 6; DB 7; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1 8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AANDEN 6
 Db 1 AANDEN 6

RESULT 7
 ADDNE3606 standard; Peptide: 9 AA.
 ID ADDNE3606 standard; Peptide: 9 AA.
 XX DT 01-JUL-2004 (first entry)
 AC ADN63606;
 XX HLA binding peptide #206.
 XX cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HLA epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KW chondyloma acuminateum.
 XX Unidentified.
 XX PN WO2004031211-A2.
 XX PD 15-APR-2004.
 XX PF 03-OCT-2003; 2003WO-US021308.
 XX PR 03-OCT-2002; 2002US-0416207P.
 XX PR 08-OCT-2002; 2002US-0417269P.
 XX PA (EPIMMUNE INC.
 XX PI Sidney J., Southwood S., Sette A;
 XX DR 2004-347953/32.

The invention relates to a novel composition comprising one or more peptides or nucleic acids encoding an HLA binding Peptide. The composition further comprises an HLA epitope. It also comprises a spacer molecule, carrier, an MHC targeting sequence or lipid. The peptides are incorporated as part of a liposome. The peptide is from an antigen selected from prostate specific antigen (PSA), prostate specific membrane antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV) antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2), Papilloma virus, Lassa virus, Mycobacterium tuberculosis (Mt), p53, murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein (rTKP). The composition is useful for preventing or treating viral infections or cancer, such as prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyloma acuminateum. The composition is also be used for diagnosing such diseases. This sequence represents a peptide of the invention.

XX Sequence 9 AA;
 SQ Query Match 45.5%; Score 5; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1 8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 YAAAV 11
 Db 5 YAAAV 9

RESULT 8
 ADD23307 standard; peptide: 14 AA.
 ID ADD23307
 XX AC ADD23307;
 XX DT 15-JAN-2004 (first entry)
 DE Breast cancer membrane protein (BCMP) peptide SEQ ID NO:556.
 XX KW breast cancer; screening; diagnosis; breast cancer therapy;
 KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX PN WO2003087831-A2.
 XX PD 23-OCT-2003.
 XX PF 10-APR-2003; 2003WO-GB001559.
 XX PR 11-APR-2002; 2002GB-00008331.
 XX PA (OXFORD GLYCOSCIENCES UK LTD.
 XX PI Hudson LJ, Stamps AC, Terrett JA;
 XX DR WPI; 2003-845381/78.
 XX PT Screening, diagnosing and/or treating breast cancer by detecting a change in expression or activity of a breast cancer membrane protein (BCMP) polypeptide or encoding nucleic acid molecule.
 XX PT Example; SEQ ID NO 556; 81PP; English.
 XX PS The present invention describes a method of screening for and/or diagnosing breast cancer in a subject, and/or monitoring the effectiveness of breast cancer therapy. The method comprises detecting and/or quantifying in a biological sample obtained from the subject a breast cancer membrane protein (BCMP) polypeptide and a nucleic acid molecule. Also described: (1) an antibody, its functional-analog, fragment, derivative or analogue, that specifically binds to one or more of the BCMP polypeptide; (2) diagnostic kit comprising a capture reagent specific for an BCMP polypeptide, reagents and instructions for use; (3) a method for screening for anti-breast cancer agents that interact with the BCMP polypeptide, comprising contacting the polypeptide with a candidate agent, and determining whether or not the candidate agent interacts with the polypeptide; (4) a method for screening for anti-breast cancer agents that modulate the expression or activity of an BCMP polypeptide or the nucleic acid molecule cited above, comprising comparing the expression or activity of the polypeptide or nucleic acid molecule, in the presence and absence of a candidate agent or in the presence of a control agent, and determining whether the candidate agent causes the expression or activity of the polypeptide or nucleic acid molecule to change; and (5) an agent identified by the method of (3) or (4), which interacts with the polypeptide or causes the expression or activity of the polypeptide, or the expression of the nucleic acid molecule to change. BCMPs have cytostatic activities, and can be used in vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or their derivatives, are useful in the manufacture of a medicament for the treatment of breast cancer, where the composition is a vaccine. The

CC present sequence represents a BCMP peptide which is used in the
CC exemplification of the present invention.
XX

SQ Sequence 14 AA;

Query Match 45.5%; Score 5; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 YAAAV 11
Db 7 YAAAV 11

RESULT 9

ADK50911 ID: ADK50911 standard; peptide; 21 AA.
XX
AC ADK50911;
XX
DN 04-NOV-2004 (first entry)
XX DE Human C35 / Kaposi FGF signal sequence MST cell-penetrating peptide 123.
XX C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma;
KW human; Kaposi FGF signal sequence h region MST; cell-penetrating;
KW fibroblast growth factor; membrane-translocating signal.
XX OS Homo sapiens.
OS Unidentified.
PN WO2003104428-A2.
XX PD 18-DEC-2003.
XX PP 10-JUN-2003; 2003WO-US018252.
XX PR 10-JUN-2002; 2002US-03867318P.
PR 11-DEC-2002; 2002US-0432211P.
PR 23-APR-2003; 2003US-0464650P.
XX PA (VACC-) VACCINEX INC.
PA (UYRP) UNIV. ROCHESTER.
XX PI Zauderer M, Evans EE, Borrello MA;
XX DR 2004-062349/06.
XX PS Novel C35 polypeptide useful for formulation of immunogenic composition
to induce antibodies and cell-mediated immunity against tumor cells.
XX Disclosure: Page 223; 626pp; English.

XX The invention relates to a novel isolated polypeptide comprising or
CC consisting of two or more C35 peptide epitopes. The polypeptide of the
CC invention demonstrates cytostatic activity and may be useful for the
CC formulation of an immunogenic composition, such as a vaccine, to induce
CC antibodies and cell-mediated immunity against target cells such as tumour
CC cells. Furthermore, the polypeptide and its analogues may be useful as
CC prognostic markers for carcinoma, such as human breast or bladder
CC carcinoma. The current sequence is that of human C35 / Kaposi FGF
CC (fibroblast growth factor) signal sequence MST (membrane-translocating
CC sequence) cell-penetrating polypeptide of the invention.

SQ Sequence 21 AA;

Query Match 45.5%; Score 5; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 YAAAV 11
Db 8 YAAAV 12

RESULT 10

ADC33576 ID: ADC33576 standard; peptide; 22 AA.
XX AC ADC33576;
XX DT 18-DEC-2003 (first entry)
XX DE Fusion peptide fragment #SEQ ID 50.
KW Fused polypeptide; autoantigen; tolerogen; neurodegenerative disease.
OS synthetic.
XX PN JP2003000264-A.
XX PD 07-JAN-2003.
PF 11-APR-2002; 2002JP-00108834.
XX PR 16-APR-2001; 2001US-00836433.
XX PA (NICH -) JAPAN CHEM RES CO LTD.
XX DR WPI; 2003-461481/44.
XX PT A hybrid protein for autoimmune diseases, a polynucleotide, an expression
PT vector, a fused polypeptide, a drug composition, a host cell, preparation
of an autoantigen fused polypeptide.
XX PS Example 6; SEQ ID NO 50; 30pp; Japanese.
XX The invention relates to a polynucleotide encoding a fused polypeptide
comprising a polynucleotide encoding at least one autoantigen peptide
fused inframe to a polynucleotide encoding a tolerogen polypeptide. Also
disclosed is an expression vector containing the above polynucleotide
linked operably to at least one transcription-controlling element, a
fused polypeptide expressed from the above expression vector, and a drug
composition containing the above fused polypeptide and
pharmacologically allowable carrier. The autoantigen fused polypeptide
can be used for treating neurodegenerative diseases. Sequences given in
records ADC3357-(seqid:13) represent fusion peptides of the invention.
CC their fragments, DNA encoding them and primers.
XX SQ Sequence 22 AA;
Query Match 45.5%; Score 5; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

AAR37123 ID: AAR37123 standard; peptide; 30 AA.
XX AC AAR37123;
XX DR 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 17-NOV-1994 (first entry)
DE Decarbamylase N-terminal fragment.
XX KW N-terminal; decarbamylase; enzyme; Comamonas; sp. E222C; Blastobacter;
KW sp. A17p4; Rhizobium; sp. KNK1415; D-alpha amino acid;
KW N-carbamyl-D-alpha-amino acid; neutral; alkaline; semi-synthetic;
KW penicillin; cephalosporin.

XX	OS	Comamonas sp; E222C.	PR	08-JUL-1997;	97US-0051916P.
XX	Key	Location/Qualifiers	PR	08-JUL-1997;	97US-0051918P.
PH	Misc-difference 20	/note= "Uncertainty regarding this position"	PR	08-JUL-1997;	97US-0051919P.
FT	Misc-difference 26	/note= "Uncertainty regarding this position"	PR	08-JUL-1997;	97US-0051925P.
FT	Misc-difference 26	/note= "Uncertainty regarding this position"	PR	08-JUL-1997;	97US-0051926P.
FT	Misc-difference 26	/note= "Uncertainty regarding this position"	PR	08-JUL-1997;	97US-0051928P.
XX	PN	WO9408030-A1.	PR	08-JUL-1997;	97US-0051929P.
XX	PD	14-APR-1994.	PR	08-JUL-1997;	97US-0051931P.
XX	PD	01-OCT-1993;	PR	08-JUL-1997;	97US-0052732P.
PF	93WO-JP001408.		PR	08-JUL-1997;	97US-0052733P.
XX	PR	05-OCT-1992;	PR	08-JUL-1997;	97US-0052735P.
XX	PA (KANSAFUCHI CHEM IND CO LTD.		PR	08-JUL-1997;	97US-0052803P.
XX	PI Yamada H, Shimizu S, Ikenaka Y, Yajima K, Yamada Y, Nanba H;		PR	18-AUG-1997;	97US-0055634P.
PI	Takano M,		PR	18-AUG-1997;	97US-0055722P.
XX	XX		PR	18-AUG-1997;	97US-0055723P.
PT	D-alpha-aminoacid prodn using decarboxylase enzyme - can be efficiently produced under neutral to alkaline conditions, giving prod useful in prodn of semi-synthetic penicillin and cephalosporin cpds.		PR	18-AUG-1997;	97US-0055947P.
PT	WPI; 1994-135591/16.		PR	18-AUG-1997;	97US-0055948P.
XX	XX		PR	18-AUG-1997;	97US-0055949P.
DR	DR		PR	18-AUG-1997;	97US-0055950P.
PT	The sequences given in AAR37123-25 represent the N-terminal fragments of the decarboxylase enzyme of the invention derived from Comamonas sp. CC222C, Blastoacter sp. Al7-p-4 and Rhizobium sp. KNK1415 respectively. These enzymes may be used in the production of D-alpha-amino acids by treating N-carbamyl-D-alpha-amino acids with the enzyme which is produced by a microorganism in an aqueous medium. The decarboxylase is efficient under neutral to alkaline conditions and may be used in the production of semi-synthetic penicillin and cephalosporin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)		PR	18-AUG-1997;	97US-0055953P.
PS	Claim 14; Page 33; 52PP; Japanese.		PR	18-AUG-1997;	97US-0055954P.
XX	XX		PR	18-AUG-1997;	97US-0055954P.
CC	CC		PR	18-AUG-1997;	97US-0055954P.
CC	CC		PR	18-AUG-1997;	97US-0055954P.
CC	CC		PR	18-AUG-1997;	97US-0055954P.
CC	CC		PR	18-AUG-1997;	97US-0055954P.
CC	CC		PR	18-AUG-1997;	97US-0055954P.
CC	CC		PR	18-AUG-1997;	97US-0055954P.
XX	XX		PR	18-AUG-1997;	97US-0055954P.
SQ	Sequence 30 AA;		PR	12-SEP-1997;	97US-0058630P.
XX	XX		PR	12-SEP-1997;	97US-0058630P.
CC	CC		PR	12-SEP-1997;	97US-0058631P.
CC	CC		PR	12-SEP-1997;	97US-0058664P.
CC	CC		PR	12-SEP-1997;	97US-0058785P.
XX	XX		PR	07-JUL-1998;	98WO-US013684.
XX	XX		PR	08-JAN-1999;	99US-00227357.
XX	XX		PA	(FISC/)	FISCHER C L.
XX	XX		PA	(ROSE/)	ROSEN C A.
XX	XX		PA	(SOPP/)	SOPPET D R.
XX	XX		PA	(RUBE/)	RUBEN S M.
XX	XX		PA	(KYAW/)	KYAW H.
XX	XX		PA	(LIIV/)	LIIV Y.
XX	XX		PA	(ZENG/)	ZENG Z.
XX	XX		PA	(LAFL/)	LAFLEUR D W.
XX	XX		PA	(MOOR/)	MOORE P A.
XX	XX		PA	(SHIV/)	SHI Y.
XX	XX		PA	(OLSE/)	OLSEN H S.
XX	XX		PA	(EBNE/)	EBNER R.
XX	XX		PA	(BREW/)	BREWER L A.
XX	XX		PI	Fischer CL, Rosan CA, Soppe	Lafleur DW, Moore PA, Shi Y
XX	XX		DR	WPI; 2003-540785/51.	
XX	XX		XX	Novel antibody which specifically binds to a protein	
XX	XX		PT	diagnosing and treating lupus	
XX	XX		PT		
XX	XX		XX	Disclosure; Page 26; 355pp; E	
XX	XX		PS		
XX	XX		XX	The invention relates to an antibody which specifically binds to a protein	
XX	XX		XX	produced by immunising an animal with a protein containing a secreted polypeptide encoded by	
XX	XX		XX	amino acid sequence of secreted	
XX	XX		XX	HLHFP03 cDNA contained in ATCC	
XX	XX		XX	produced by immunising an animal with a protein containing a secreted polypeptide encoded by	
XX	XX		XX	ADA07417, or with a protein containing a secreted polypeptide encoded by	
XX	XX		XX	Deposit No. 209126, respectively	
XX	XX		XX	produces the antibody and a monoclonal antibody is a monoclonal, polyclonal	
XX	XX		XX	antibody	

antibody. Optionally, the antibody is a Fab fragment, and is labelled by a label chosen from enzyme label, a radioisotope, and a fluorescent label. The antibody is useful as a probe for differential identification of tissues or cell types in which Ab07417 is expressed. The antibody is also for diagnosis and treatment of autoimmune diseases and disorders, such as lupus, transplant rejection, allergic reactions, and arthritis.

The present sequence is a peptide/protein derived from one of the 123 novel secreted proteins.

Sequence 31 AA;

Query Match 45.5%; Score 5; DB 7; Length 31;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10
Db 14 NYAAA 18

RESULT 13

ID ADN41386 Standard; peptide: 31 AA.

XX ADN41386;

XX DT 17-JUN-2004 (first entry)

Novel human secreted protein fragment seqid 508.
KW immunomodulator; immunosuppressive; antiinflammatory; dermatological; antiarthritic; antirheumatic; neuroprotective; antianæmic; muscular; antiallergic; antiasthmatic; gastrointestinal; anticoagulant; thrombotic; antiarteriosclerotic; cardiotropic; nephrotropic; cardiovascular; respiratory; cardiant; cytostatic; nephrotropic; chromosome identification; gene therapy; secreted protein; immune system disorder; immunodeficiency; hybrid mapping; gene expression control; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; haemolytic anaemia; myasthenia gravis; allergic reaction; asthma; inflammatory condition; inflammatory bowel disease; B cell stimulator; T cell activator; blood-related disorder; eosinophilia; thrombosis; thromboembolism; atherosclerosis; myocardial infarction; angina; anaemia; hyperproliferative disorder; cancer; renal disorder; chronic kidney failure; renal tubular acidosis; kidney stone; cardiovascular disorder; respiratory disorder; human.

Homo sapiens:

OS US2004044191-A1.

XX PD 04-MAR-2004.

PP 10-OCT-2001; 2001US-00973278.

XX PR 08-JUL-1997; 97US-0051916P.

PR 08-JUL-1997; 97US-0051918P.

PR 08-JUL-1997; 97US-0051920P.

PR 08-JUL-1997; 97US-0051925P.

PR 08-JUL-1997; 97US-0051926P.

PR 08-JUL-1997; 97US-0051928P.

PR 08-JUL-1997; 97US-0051929P.

PR 08-JUL-1997; 97US-0052733P.

PR 08-JUL-1997; 97US-0052739P.

PR 08-JUL-1997; 97US-0052755P.

PR 08-JUL-1997; 97US-0052803P.

PR 18-AUG-1997; 97US-0055644P.

PR 18-AUG-1997; 97US-0055722P.

Sequence 31 AA;
Query Match 45.5%; Score 5; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NYAAA 10
Db 14 NYAAA 18

XX WO200100814-A2.
PN
XX 04-JAN-2001.
PD
XX 26-JUN-2000; 2000WO-EP005922.
PF
XX 25-JUN-1999; 99US-00344096.
PR
XX (UYU-) UNIV ZUERICH.
PA
PI Plueckthun A, Arndt K, Mueller K, Pelletier J;
XX DR WPI; 2001-137954/14.

XX Identifying heteroassociating (poly)peptides involves designing an appropriate coiled-coil library and screening by using a library versus library approach.

XX Claim 6; Page 41; 56pp; English.

XX The present invention relates to a method for identifying hetero-associating coiled-coil peptides. The method comprises providing a library of peptides with the general formula of AAB61546, and a second library of peptides with the general formula of AAB61547. Hetero-association of peptides can then be screened for via a screenable or selectable property caused by the hetero-association of the two peptides. The identified peptides can be used for heterodimerisation of fusion proteins. The present sequence is a hetero-associating peptide that can be used in method of the present invention

PS Sequence 32 AA;

Query Match 45.5%; Score 5; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.9e+0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DENYA 8
Db 13 DENYA 17

XX Search completed: May 5, 2005, 18:18:04
CC Job time : 104.333 secs

PS Sequence 32 AA;

Query Match 45.5%; Score 5; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.9e+0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DENYA 8
Db 13 DENYA 17

RESULT 15
ID AAB61569 standard; peptide: 32 AA.
XX AAB61569;
AC
XX DT 03-APR-2001 (first entry)
DB Peptide WINZIPB11 used to identify hetero-associating peptides.
XX Hetero-associating coiled-coil peptide; heterodimerisation.
XX Unidentified.